

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 15:26:55 ; Search time 1325 Seconds
(without alignments)
2257.109 Million cell updates/sec

Title: US-09-719-533a-1_COPY_527_595

Perfect score: 69

Sequence: 1 ACAATCTGCTCAGGAAC.....AACCTACGACAGAACTGC 69

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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33: em_htg_mus.*
34: em_htg_pin.*
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37: em_htg_vrt.*
38: em_sv.*
39: em_hngo_hum.*
40: em_hngo_mus.*
41: em_hngo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	69	100.0	192	14	AF198767	AF198767 Hepatitis
2	69	100.0	3215	6	BD232230	BD232230 Hepatitis
3	67.4	97.7	192	14	AF198698	AF198698 Hepatitis
4	67.4	97.7	192	14	AF198704	AF198704 Hepatitis
5	67.4	97.7	192	14	AF198705	AF198705 Hepatitis
6	67.4	97.7	192	14	AF198706	AF198706 Hepatitis
7	67.4	97.7	192	14	AF198707	AF198707 Hepatitis
8	67.4	97.7	192	14	AF198708	AF198708 Hepatitis
9	67.4	97.7	192	14	AF198709	AF198709 Hepatitis
10	67.4	97.7	192	14	AF198710	AF198710 Hepatitis
11	67.4	97.7	192	14	AF198711	AF198711 Hepatitis
12	67.4	97.7	192	14	AF198712	AF198712 Hepatitis
13	67.4	97.7	192	14	AF198713	AF198713 Hepatitis
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15	67.4	97.7	192	14	AF198715	AF198715 Hepatitis
16	67.4	97.7	192	14	AF198716	AF198716 Hepatitis
17	67.4	97.7	192	14	AF198717	AF198717 Hepatitis
18	67.4	97.7	192	14	AF198718	AF198718 Hepatitis
19	67.4	97.7	192	14	AF198721	AF198721 Hepatitis
20	67.4	97.7	192	14	AF198722	AF198722 Hepatitis
21	67.4	97.7	192	14	AF198723	AF198723 Hepatitis
22	67.4	97.7	192	14	AF198724	AF198724 Hepatitis
23	67.4	97.7	192	14	AF198725	AF198725 Hepatitis
24	67.4	97.7	192	14	AF198726	AF198726 Hepatitis
25	67.4	97.7	192	14	AF198727	AF198727 Hepatitis
26	67.4	97.7	192	14	AF198734	AF198734 Hepatitis
27	67.4	97.7	192	14	AF198735	AF198735 Hepatitis
28	67.4	97.7	192	14	AF198736	AF198736 Hepatitis
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36	67.4	97.7	192	14	AF198744	AF198744 Hepatitis
37	67.4	97.7	192	14	AF198745	AF198745 Hepatitis
38	67.4	97.7	192	14	AF198746	AF198746 Hepatitis
39	67.4	97.7	192	14	AF198747	AF198747 Hepatitis
40	67.4	97.7	192	14	AF198748	AF198748 Hepatitis
41	67.4	97.7	192	14	AF198749	AF198749 Hepatitis
42	67.4	97.7	192	14	AF198750	AF198750 Hepatitis
43	67.4	97.7	192	14	AF198751	AF198751 Hepatitis
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ALIGNMENTS

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DEFINITION Hepatitis B virus isolate CCN41 surface antigen gene, partial cds.
ACCESSION AF198767
VERSION AF198767.1 GI:6537407
KEYWORDS
SOURCE
ORGANISM
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE
1 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL Unpublished

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REFERENCE 2 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 36 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 95
QY 61 AGAAACTGC 69
Db 96 AGAAACTGC 104

RESULT 2
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LOCUS Hepatitis B virus strains appearing by vaccine administration and
DEFINITION utilization thereof.
ACCESSION BD232230
VERSION BD232230.1 GI:33042000
KEYWORDS JP 2002518013-A/1.
SOURCE unidentifed
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 3215)
AUTHORS Oon,C.J., Lim,G.K., Leong,A.L., Zhao,Y. and Chen,W.N.
TITLE Hepatitis B virus strains appearing by vaccine administration and utilization thereof
JOURNAL Patent: JP 2002518013-A 1 25-JUN-2002;
GOVERNMENT OF THE REPUBLIC OF SINGAPORE
COMMENT OS Unidentified
PN JP 2002518013-A/1
PD 25-JUN-2002
PF 19-JUN-1998 JP 2000554856
PI CHONG JIN OON,GEK KEOW LIM, AI LIN LEONG, YI ZHAO, WEI NING CHEN
PC C12N15/09,A61K39/29,A61K45/00,A61P1/16,A61P31/20,A61P35/00,PC C07K14/02,
PC C07K16/08,C12N7/00,C12P21/02,C12P21/08,C12P1/68,G01N33/53,PC G01N33/53,
PC G01N33/56,G01N33/576,C12N15/00
CC Strandedness: Double;
CC Topology: Circular;
CC Hepatitis B virus strains appearing by vaccine administration and utilization thereof
CC utilization thereof
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FT source /organism='Unidentified'.
FT Location/Qualifiers

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QY 61 AGAAACTGC 69
Db 587 AGAAACTGC 595

RESULT 3
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DEFINITION Hepatitis B virus
ACCESSION AF198698
VERSION AF198698.1 GI:6537338
KEYWORDS Hepatitis B virus
SOURCE Hepatitis B virus
ORGANISM Hepatitis B virus
REFERENCE 1 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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Best Local Similarity 98.6%; Pred. No. 1.7e-14;
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QY 61 AGAAACTGC 69
Db 96 AGAAACTGC 104

RESULT 4
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LOCUS      AF198704      192 bp      DNA      linear      VRL 08-DEC-1999
DEFINITION Hepatitis B virus isolate CCC57 surface antigen gene, partial cds.
ACCESSION   AF198704
VERSION     AF198704.1 GI:6537344
SOURCE      Hepatitis B virus
ORGANISM    Hepatitis B virus
REFERENCE   1 (bases 1 to 192)
AUTHORS     Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE       Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 192)
AUTHORS     Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE       Direct Submission
JOURNAL     Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
FEATURES   Location/Qualifiers
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QY 61 AGAAACTGC 69
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Db 96 GGAAACTGC 104

RESULT 5
LOCUS      AF198705      192 bp      DNA      linear      VRL 08-DEC-1999
DEFINITION Hepatitis B virus isolate CCC58 surface antigen gene, partial cds.
ACCESSION   AF198705
VERSION     AF198705.1 GI:6537345
SOURCE      Hepatitis B virus
ORGANISM    Hepatitis B virus
REFERENCE   1 (bases 1 to 192)
AUTHORS     Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE       Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 192)
AUTHORS     Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE       Direct Submission
JOURNAL     Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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Db 36 ACAACTCCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 95

QY 61 AGAAACTGC 69
    |||||
Db 96 GGAAACTGC 104

RESULT 6
LOCUS      AF198706      192 bp      DNA      linear      VRL 08-DEC-1999
DEFINITION Hepatitis B virus isolate CCC59 surface antigen gene, partial cds.
ACCESSION   AF198706
VERSION     AF198706.1 GI:6537346
SOURCE      Hepatitis B virus
ORGANISM    Hepatitis B virus
REFERENCE   1 (bases 1 to 192)
AUTHORS     Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE       Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 192)
AUTHORS     Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE       Direct Submission
JOURNAL     Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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Db 96 GGAAACTGC 104

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RESULT 7
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ACCESSION  AF198707
VERSION     AF198707.1  GI:6537347
KEYWORDS
SOURCE     Hepatitis B virus
ORGANISM   Hepatitis B virus
REFERENCE  1  (bases 1 to 192)
AUTHORS    Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and
Margolis,H.S.
TITLE      Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL    Unpublished
REFERENCE  2  (bases 1 to 192)
AUTHORS    Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and
Margolis,H.S.
DIRECT SUBMISSION
SUBMITTED  (26-OCT-1999) Division of Viral and Rickettsial Disease,
National Center for Infectious Diseases, CDC, 1600 Clifton Road NE,
MS-A33, Atlanta, GA 30333, USA
MS-A33, Atlanta, GA 30333, USA
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QY      61  AGAAACTGC 69
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Db      96  GGAAACTGC 104

RESULT 9
AF198709
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DEFINITION
ACCESSION  AF198709
VERSION     AF198709.1  GI:6537349
KEYWORDS
SOURCE     Hepatitis B virus
ORGANISM   Hepatitis B virus
REFERENCE  1  (bases 1 to 192)
AUTHORS    Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and
Margolis,H.S.
TITLE      Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL    Unpublished
REFERENCE  2  (bases 1 to 192)
AUTHORS    Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and
Margolis,H.S.
DIRECT SUBMISSION
SUBMITTED  (26-OCT-1999) Division of Viral and Rickettsial Disease,
National Center for Infectious Diseases, CDC, 1600 Clifton Road NE,
MS-A33, Atlanta, GA 30333, USA
MS-A33, Atlanta, GA 30333, USA
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QY      61  AGAAACTGC 69
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Db      96  GGAAACTGC 104

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DEFINITION
ACCESSION  AF198708
VERSION     AF198708.1  GI:6537348
KEYWORDS
SOURCE     Hepatitis B virus
ORGANISM   Hepatitis B virus
REFERENCE  1  (bases 1 to 192)
AUTHORS    Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and
Margolis,H.S.

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TITLE      Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL    Unpublished
REFERENCE  2  (bases 1 to 192)
AUTHORS    Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and
Margolis,H.S.
DIRECT SUBMISSION
SUBMITTED  (26-OCT-1999) Division of Viral and Rickettsial Disease,
National Center for Infectious Diseases, CDC, 1600 Clifton Road NE,
MS-A33, Atlanta, GA 30333, USA
MS-A33, Atlanta, GA 30333, USA
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Best Local Similarity 98.6%; Pred. No. 1.7e-14;
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QY      61  AGAAACTGC 69
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Db      96  GGAAACTGC 104

RESULT 9
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LOCUS      Hepatitis B virus isolate CCG60 surface antigen gene, partial cds.
DEFINITION
ACCESSION  AF198709
VERSION     AF198709.1  GI:6537349
KEYWORDS
SOURCE     Hepatitis B virus
ORGANISM   Hepatitis B virus
REFERENCE  1  (bases 1 to 192)
AUTHORS    Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and
Margolis,H.S.
TITLE      Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL    Unpublished
REFERENCE  2  (bases 1 to 192)
AUTHORS    Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and
Margolis,H.S.
DIRECT SUBMISSION
SUBMITTED  (26-OCT-1999) Division of Viral and Rickettsial Disease,
National Center for Infectious Diseases, CDC, 1600 Clifton Road NE,
MS-A33, Atlanta, GA 30333, USA
MS-A33, Atlanta, GA 30333, USA
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ORIGIN

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Best Local Similarity 98.6%; Pred. No. 1.7e-14;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
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Db 36 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 95
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QY 61 AGAAACTGC 69
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Db 96 GGAACCTGC 104
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RESULT 10
AF198710
LOCUS
DEFINITION Hepatitis B virus isolate CCC62 surface antigen gene, partial cds.
ACCESSION AF198710
VERSION AF198710.1 GI:6537350
KEYWORDS
SOURCE
ORGANISM Hepatitis B virus
REFERENCE 1 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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Query Match 97.7%; Score 67.4; DB 14; Length 192;
Best Local Similarity 98.6%; Pred. No. 1.7e-14;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 AGAAACTGC 69
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RESULT 11
AF198711
LOCUS
DEFINITION Hepatitis B virus isolate CCC64 surface antigen gene, partial cds.
ACCESSION AF198711
VERSION AF198711.1 GI:6537351
KEYWORDS
SOURCE
ORGANISM Hepatitis B virus
REFERENCE 1 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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DEFINITION Hepatitis B virus isolate CCC64 surface antigen gene, partial cds.
ACCESSION AF198711
VERSION AF198711.1 GI:6537351
KEYWORDS
SOURCE
ORGANISM Hepatitis B virus
REFERENCE 1 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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Best Local Similarity 98.6%; Pred. No. 1.7e-14;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
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Db 36 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 95
|||||

QY 61 AGAAACTGC 69
|||||
Db 96 GGAACCTGC 104
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RESULT 12

AF198712
LOCUS
DEFINITION Hepatitis B virus isolate CCC70 surface antigen gene, partial cds.
ACCESSION AF198712
VERSION AF198712.1 GI:6537352
KEYWORDS
SOURCE
ORGANISM Hepatitis B virus
REFERENCE 1 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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RESULT 13
AF198713
LOCUS
DEFINITION
Hepatitis B virus isolate CCC71 surface antigen gene, partial cds.
ACCESSION
AF198713
VERSION
AF198713.1 GI:6537353
SOURCE
Hepatitis B virus
ORGANISM
Hepatitis B virus
REFERENCE
1 (bases 1 to 192)
Xia, G.-L., Nainan, O.V., Jia, Z.-Y., Cao, H.-L., Liu, C.-B. and Margolis, H.S.
DISTRIBUTION of hepatitis B virus subtypes and genotypes in China
Unpublished
2 (bases 1 to 192)
Xia, G.-L., Nainan, O.V., Jia, Z.-Y., Cao, H.-L., Liu, C.-B. and Margolis, H.S.
Direct Submission
Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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Db 36 ACAAACCTCTGCTCAAGGACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 95

Qy 61 AGAAACTGC 69
Db 96 GGAAACTGC 104

RESULT 14
AF198714
LOCUS
DEFINITION
Hepatitis B virus isolate CCC79 surface antigen gene, partial cds.
ACCESSION
AF198714
VERSION
AF198714.1 GI:6537354
SOURCE
Hepatitis B virus
ORGANISM
Hepatitis B virus
REFERENCE
1 (bases 1 to 192)
Xia, G.-L., Nainan, O.V., Jia, Z.-Y., Cao, H.-L., Liu, C.-B. and Margolis, H.S.
DISTRIBUTION of hepatitis B virus subtypes and genotypes in China
Unpublished
2 (bases 1 to 192)
Xia, G.-L., Nainan, O.V., Jia, Z.-Y., Cao, H.-L., Liu, C.-B. and Margolis, H.S.
Direct Submission
Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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Qy 61 AGAAACTGC 69
Db 96 GGAAACTGC 104

RESULT 15
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LOCUS
DEFINITION
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ACCESSION
AF198715
VERSION
AF198715.1 GI:6537355
SOURCE
Hepatitis B virus
ORGANISM
Hepatitis B virus
REFERENCE
1 (bases 1 to 192)
Xia, G.-L., Nainan, O.V., Jia, Z.-Y., Cao, H.-L., Liu, C.-B. and Margolis, H.S.
DISTRIBUTION of hepatitis B virus subtypes and genotypes in China
Unpublished
2 (bases 1 to 192)
Xia, G.-L., Nainan, O.V., Jia, Z.-Y., Cao, H.-L., Liu, C.-B. and Margolis, H.S.
Direct Submission
Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACAAACCTCTGCTCAAGGACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60

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Db 36 ACAAACCTCTGCTCAAGGACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 95

Qy 61 AGAAACTGC 69
Db 96 GGAAACTGC 104

RESULT 14
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DEFINITION
Hepatitis B virus isolate CCC79 surface antigen gene, partial cds.
ACCESSION
AF198714
VERSION
AF198714.1 GI:6537354
SOURCE
Hepatitis B virus
ORGANISM
Hepatitis B virus
REFERENCE
1 (bases 1 to 192)
Xia, G.-L., Nainan, O.V., Jia, Z.-Y., Cao, H.-L., Liu, C.-B. and Margolis, H.S.
DISTRIBUTION of hepatitis B virus subtypes and genotypes in China
Unpublished
2 (bases 1 to 192)
Xia, G.-L., Nainan, O.V., Jia, Z.-Y., Cao, H.-L., Liu, C.-B. and Margolis, H.S.
Direct Submission
Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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Qy 61 AGAAACTGC 69
Db 96 GGAAACTGC 104

RESULT 15
AF198715
LOCUS
DEFINITION
Hepatitis B virus isolate CCC80 surface antigen gene, partial cds.
ACCESSION
AF198715
VERSION
AF198715.1 GI:6537355
SOURCE
Hepatitis B virus
ORGANISM
Hepatitis B virus
REFERENCE
1 (bases 1 to 192)
Xia, G.-L., Nainan, O.V., Jia, Z.-Y., Cao, H.-L., Liu, C.-B. and Margolis, H.S.
DISTRIBUTION of hepatitis B virus subtypes and genotypes in China
Unpublished
2 (bases 1 to 192)
Xia, G.-L., Nainan, O.V., Jia, Z.-Y., Cao, H.-L., Liu, C.-B. and Margolis, H.S.
Direct Submission
Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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Best Local Similarity 98.6%; Pred. No. 1.7e-14;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACAAACCTCTGCTCAAGGACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60

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JOURNAL Unpublished
REFERENCE 2 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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QY 61 AGAAACTGC 69
DB |||||||
96 GGAAGACTGC 104

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Job time : 1326 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 15:25:30 ; Search time 199 Seconds
(without alignments)
1472.993 Million cell updates/sec

Title: US-09-719-533A-1_COPY_527_595

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Sequence: 1 AACACTCCCTCCTCAGGAC.....AACCTACGACAGAACTGC 69

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
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- 7: Geneseq2003as.*
- 8: Geneseq2003bs.*
- 9: Geneseq2003cs.*
- 10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	67.4	97.7	687	2	Aaq98179 Hepatitis
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4	65.8	95.4	297	4	Aaf56121 HBV DNA p
5	65.8	95.4	297	4	Aaf56122 HBV DNA p
6	65.8	95.4	297	4	Aaf56123 HBV DNA p
7	65.8	95.4	297	4	Aaf56120 HBV DNA p
8	65.8	95.4	297	4	Aaf56127 HBV DNA p
9	65.8	95.4	297	4	Aaf56128 HBV DNA p
10	65.8	95.4	306	9	Add4437 RNA virus
11	65.8	95.4	426	3	Aad00819 Hepatitis
12	65.8	95.4	426	3	Aad14305 Hepatitis
13	65.8	95.4	477	2	Aat58385 Hepatitis
14	65.8	95.4	684	2	Aaq75318 Mutant He
15	64.2	93.0	426	3	Aad00829 Hepatitis
16	64.2	93.0	426	4	Aad14315 Hepatitis
17	62.6	90.7	3220	3	Aaz88924 Hepatitis
18	61	88.4	297	4	Aaf56108 HBV DNA p
19	61	88.4	297	4	Aaf56131 HBV DNA p
20	61	88.4	297	4	Aaf56126 HBV DNA p
21	61	88.4	297	4	Aaf56119 HBV DNA p
22	61	88.4	297	4	Aaf56124 HBV DNA p
23	61	88.4	297	4	Aaf56109 HBV DNA p

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26	61	88.4	426	3	Aad00825
27	61	88.4	426	3	Aad00826
28	61	88.4	426	4	Aad14312
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31	61	88.4	671	4	Aaf26964
32	61	88.4	671	7	Abq80939
33	61	88.4	681	2	Aav42306
34	61	88.4	681	3	Ab152852
35	61	88.4	681	3	Ab152852
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ALIGNMENTS

RESULT 1

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ID AAZ29453 standard; DNA; 3215 BP.

AC AAZ29453;

DT 06-AUG-2003 (revised)

DT 14-MAR-2000 (first entry)

XX Mutant hepatitis B viral genome.

XX HBIG; Hepatitis B immunoglobulin; HBV; Hepatitis B virus;

XX mutant major surface antigen; human hepatitis B viral genome;

XX human hepatitis B virus surface antigen- 'S'- 145 Singapore strain;

XX hepatocellular carcinoma; HBV infection; circular; cyclic; ds.

XX Hepatitis B virus.

XX Key Location/Qualifiers

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FT /product= "Trans-activating X protein"

FT CDS 1814..2452

FT /tag= c

FT /product= "Core protein sequence"

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FT /transl_except= (pos:2904..2906,glu)

FT /note= "Partial sequence of DNA polymerase antigen"

FT mat_peptide 2848..3213

FT /tag= b

FT /note= "Partial human hepatitis B virus large antigen"

XX WO9966047-A1.

PN 23-DEC-1999.

XX 19-JUN-1998; 98WO-SG0000045.

PD 19-JUN-1998; 98WO-SG0000045.

XX (GOVE-) GOVERNMENT REPUBLIC SINGAPORE.

PA Oon CJ, Lim GK, Leong AL, Zhao Y, Chen WN;

XX

DR WPI; 2000-106103/09.
 DR P-PSDB; AAY44348, AAY44349, AAY44350, AAY44351.
 PT New vaccine-escape mutant of hepatitis B virus and related proteins,
 PT nucleic acids and antibodies, useful for diagnosis, prevention and
 PT treatment.
 XX Claim 3; Fig 3; 65pp; English.
 PS
 CC The present sequence encodes 4 overlapping reading frames of mutant human
 CC hepatitis B viral genome. This was isolated from a male, 11 year old
 CC Singaporean child which had received standard HBIG and HB vaccine and was
 CC infected with the mutated strain designated human hepatitis B virus
 CC surface antigen- 'S'- 145 Singapore strain, a year later. This DNA is
 CC used for recombinant production of mutant major surface antigen and as a
 CC source of diagnostic oligonucleotides. The mutated major surface antigen
 CC is used to raise specific antibodies, to identify specific binding agents
 CC and, in vaccines or compositions for treatment or prevention of HBV
 CC infection and hepatocellular carcinoma. Antibodies are used in diagnosis
 CC or for screening donated body fluids or tissues. (Updated on 06-AUG-2003
 CC to correct OS field.)
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 Query Match 100.0%; Score 69; DB 3; Length 3215;
 Best Local Similarity 100.0%; Pred. No. 1.9e-15;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
 DB 527 ACAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 586
 QY 61 AGAAACTGC 69
 DB 587 AGAAACTGC 595
 RESULT 2
 AAQ98179
 ID AAQ98179 standard; DNA; 687 BP.
 XX AC
 AC AAQ98179;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 19-DEC-1995 (first entry)
 XX
 DE Hepatitis B virus surface antigen protein (mHBsAg) isolate 1.
 XX
 KW Hepatitis B virus; surface antigen; envelope region; 'a' determinant; ss.
 XX
 OS Hepatitis B virus; isolate 1.
 XX
 FH Key Location/Qualifiers
 FT variation 367..372
 FT /*tag= a
 FT /label= insertion
 XX
 PN WO9521189-A1.
 XX
 PD 10-AUG-1995.
 XX
 PF 02-FEB-1995; 95WO-GB000208.
 XX
 PR 02-FEB-1994; 94GB-00001987.
 XX
 PA (UNLO) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.
 XX
 PI Karayannis P, Thomas HC;
 DR WPI; 1995-283727/37.
 XX
 PT New mutant hepatitis B surface antigen - used for the detection

prevention and treatment of hepatitis B infection.
 Claim 10; Fig 6; 39pp; English.
 Two Chinese patients with hepatitis were studied. Patient No. 1 was a 58
 year old male, with a 6 year history of non-A, non-B chronic hepatitis.
 HBV-DNA was found by PCR in the absence of HBeAg and other HBV markers at
 a time when the patient had cirrhosis. Patient No. 2 was a 23 year old
 woman from the south of China who on routine testing had a slightly
 elevated serum aminotransferase (ALT) level and was positive for HBeAg
 and HBeAg, but negative for both immunoglobulin (Ig) M and IgG anti-HBs.
 On follow-up she continued to be HBV-DNA positive and was also anti-HB
 positive but negative for HBeAg, HBeAg and anti-HBs. Both patients were
 negative for hepatitis C virus (HVC) and HVC-RNA. DNA was isolated from
 serum samples and used as a template for PCR amplification. Primers M3
 and 3C (see AAQ98187 & AAQ98188) were used to amplify the Pre-C and C
 regions. Direct sequencing of the PCR products was carried out using
 sequencing primers AAQ98181-Q98186. The S genes consist of 687 bp in
 isolate 1, 690 bp in isolate 2 and 681 bp in the wild types. The S
 nucleotide and AA sequences of the mutants were compared with a published
 sequence of the same subtype (adv) and also with a wild type strain from
 an HBeAg-positive carrier from the same region. Sequencing results
 revealed an insertion in the S gene. Inserted sequences encode two
 additional AAs (Arg-Ala) between codons 122 and 123 in isolate 1, and
 three additional AAs (Arg-Gly-Ala) between codons 123 and 124 in isolate
 2. These insertions occur immediately before the 'a' determinant of
 HBeAg. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-
 2003 to standardise OS field)
 SQ Sequence 687 BP; 139 A; 184 C; 144 G; 220 T; 0 U; 0 Other;
 Query Match 97.7%; Score 67.4; DB 2; Length 687;
 Best Local Similarity 98.6%; Pred. No. 4.8e-15;
 Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
 DB 379 ACAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 438
 QY 61 AGAAACTGC 69
 DB 439 GGAAACTGC 447
 RESULT 3
 AAQ98180
 ID AAQ98180 standard; DNA; 690 BP.
 XX AC
 AC AAQ98180;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 19-DEC-1995 (first entry)
 XX
 DE Hepatitis B virus surface antigen protein (mHBsAg) isolate 2.
 XX
 KW Hepatitis B virus; surface antigen; envelope region; 'a' determinant; ss.
 XX
 OS Hepatitis B virus; isolate 2.
 XX
 FH Key Location/Qualifiers
 FT variation 368..376
 FT /*tag= a
 FT /label= insertion
 XX
 PN WO9521189-A1.
 XX
 PD 10-AUG-1995.
 XX
 PF 02-FEB-1995; 95WO-GB000208.
 XX
 PR 02-FEB-1994; 94GB-00001987.
 XX

(UNLO) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.

Karayianis P, Thomas HC;
WPI; 1995-283727/37.

New mutant hepatitis B surface antigen - used for the detection
prevention and treatment of hepatitis B infection.

Claim 10; Fig 7; 39pp; English.

Two Chinese patients with hepatitis were studied. Patient No. 1 was a 58
year old male, with a 6 year history of non-A, non-B chronic hepatitis.
HBV-DNA was found by PCR in the absence of HBeAg and other HBV markers at
a time when the patient had cirrhosis. Patient No. 2 was a 21 year old
woman from the south of China who on routine testing had a slightly
elevated serum aminotransferase (ALT) level and was positive for HBeAg
and HBeAg, but negative for both immunoglobulin (Ig) M and IgG anti-HBs.
On follow-up she continued to be HBV-DNA positive and was also anti-HB
positive but negative for HBeAg, HBeAg and anti-HBs. Both patients were
negative for hepatitis C virus (HVC) and HVC-RNA. DNA was isolated from
serum samples and used as a template for PCR amplification. Primers M3
and 3C (see AAQ98187 & AAQ98188) were used to amplify the Pre-C and C
regions. Direct sequencing of the PCR products was carried out using
sequencing primers AAQ98181-Q98186. The S genes consist of 687 bp in
isolate 1, 690 bp in isolate 2 and 681 bp in the wild types. The S
nucleotide and AA sequences of the mutants were compared with a published
sequence of the same subtype (adw) and also with a wild type strain from
an HBeAg-positive carrier from the same region. Sequencing results
revealed an insertion in the S gene. Inserted sequences encode two
additional AAs (Arg-Ala) between codons 122 and 123 in isolate 1, and
three additional AAs (Arg-Gly-Ala) between codons 123 and 124 in isolate
2. These insertions occur immediately before the 'a' determinant of
HBeAg. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-
2003 to standardise OS field)

Sequence 690 BP; 140 A; 186 C; 145 G; 219 T; 0 U; 0 Other;
Query Match 97.7%; Score 67.4; DB 2; Length 690;
Best Local Similarity 98.6%; Pred. No. 4.8e-15;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ACAACTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 60
382 ACAACTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 441

61 AGAACTGC 69
442 GGAACTGC 450

RESULT 4
AAF56121
ID AAF56121 standard; DNA; 297 BP.
AAF56121;
18-APR-2001 (first entry)
HBV DNA polymerase sequence genotype 3811.
HBV; hepatitis B virus; DNA polymerase gene; anti-HBV drug resistance;
mutation detection; ds.
Hepatitis B virus.
WO200104358-A2.
18-JAN-2001.
05-JUL-1999; 99EP-00870148.
05-JUL-2000; 2000WO-EF006306.
08-JUL-1999; 99EP-00870148.

13-JUL-1999; 99US-0143546P.
(INNO-) INNOGENETICS NV.
Stuyver L, Maertens G, Van Geyt C;
WPI; 2001-138370/14.
Monitoring anti-HBV drug resistance by genetic detection of mutations in
DNA polymerase of HBV in patient's sample, involves hybridizing the
polynucleic acids of the sample with a probe and detecting the hybrid.

Claim 16; Fig 1; 64pp; English.

The present sequence is the sequence of the DNA polymerase gene from a
strain of hepatitis B virus (HBV). It is given in a specification
relating to a method for monitoring anti-HBV drug resistance in a patient
by genetic detection of any one of mutations L528M, M552V/I and/or
V/L/M555I in HBV DNA polymerase in a biological sample from the patient.
The method is useful in the field of genetic detection of anti-HBV drug
resistance during HBV therapy. The method is rapid, reliable and precise

Sequence 297 BP; 65 A; 81 C; 64 G; 87 T; 0 U; 0 Other;
Query Match 95.4%; Score 65.8; DB 4; Length 297;
Best Local Similarity 97.1%; Pred. No. 1.5e-14;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0

1 ACAACTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 60
50 ACAACTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 109

61 AGAACTGC 69
110 GGAACTGC 118

RESULT 5
AAF56122
ID AAF56122 standard; DNA; 297 BP.
AAF56122;
18-APR-2001 (first entry)
HBV DNA polymerase sequence genotype 3774.
HBV; hepatitis B virus; DNA polymerase gene; anti-HBV drug resistance;
mutation detection; ds.
Hepatitis B virus.
WO200104358-A2.
18-JAN-2001.
05-JUL-2000; 2000WO-EF006306.
08-JUL-1999; 99EP-00870148.
13-JUL-1999; 99US-0143546P.
(INNO-) INNOGENETICS NV.
Stuyver L, Maertens G, Van Geyt C;
WPI; 2001-138370/14.
Monitoring anti-HBV drug resistance by genetic detection of mutations in
DNA polymerase of HBV in patient's sample, involves hybridizing the
polynucleic acids of the sample with a probe and detecting the hybrid.

Claim 16; Fig 1; 64pp; English.


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XX 18-APR-2001 (first entry)
XX HBV DNA polymerase sequence genotype 4132.
DE
XX
XX HBV; hepatitis B virus; DNA polymerase gene; anti-HBV drug resistance;
KW mutation detection; ds.
XX
XX Hepatitis B virus.
OS
XX
XX WO200104358-A2.
PN
XX
XX 18-JAN-2001.
PD
XX
XX 05-JUL-2000; 2000WO-EP006306.
XX
XX 08-JUL-1999; 99EP-00870148.
PR
XX 13-JUL-1999; 99US-0143546P.
XX
XX (INNO-) INNOGENETICS NV.
PA
XX
XX Stuyver L, Maertens G, Van Geyt C;
PI
XX
XX WPI; 2001-138370/14.
DR
XX
XX Monitoring anti-HBV drug resistance by genetic detection of mutations in
PT DNA polymerase of HBV in patient's sample, involves hybridizing the
PT polynucleic acids of the sample with a probe and detecting the hybrid.
XX
XX Claim 16; Fig 1; 64pp; English.
XX
XX The present sequence is the sequence of the DNA polymerase gene from a
CC strain of hepatitis B virus (HBV). It is given in a specification
CC relating to a method for monitoring anti-HBV drug resistance in a patient
CC by genetic detection of any one of mutations L528M, M552V/I and/or
CC V/L/M551 in HBV DNA polymerase in a biological sample from the patient.
CC The method is useful in the field of genetic detection of anti-HBV drug
CC resistance during HBV therapy. The method is rapid, reliable and precise
XX
XX Sequence 297 BP; 63 A; 82 C; 65 G; 87 T; 0 U; 0 Other;
SQ
Query Match 95.4%; Score 65.8; DB 4; Length 297;
Best Local Similarity 97.1%; Pred. No. 1.5e-14;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAACCTACGGAC 60
DB 50 ACGACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAACCTACGGAC 109
QY 61 AGAAACTGC 69
DB 110 GGAAACTGC 118

RESULT 9
AAF56128
ID AAF56128 standard; DNA; 297 BP.
XX
XX AAF56128;
AC
XX
XX 18-APR-2001 (first entry)
DT
XX
XX HBV DNA polymerase sequence genotype 4135.
DE
XX
XX HBV; hepatitis B virus; DNA polymerase gene; anti-HBV drug resistance;
KW mutation detection; ds.
XX
XX Hepatitis B virus.
OS
XX
XX WO200104358-A2.
PN
XX
XX 18-JAN-2001.
PD
XX
XX 05-JUL-2000; 2000WO-EP006306.
XX
XX 08-JUL-1999; 99EP-00870148.
PR
XX 13-JUL-1999; 99US-0143546P.
XX
XX (INNO-) INNOGENETICS NV.
PA
XX
XX Stuyver L, Maertens G, Van Geyt C;
PI
XX
XX WPI; 2001-138370/14.
DR
XX
XX Monitoring anti-HBV drug resistance by genetic detection of mutations in
PT DNA polymerase of HBV in patient's sample, involves hybridizing the
PT polynucleic acids of the sample with a probe and detecting the hybrid.
XX
XX Claim 16; Fig 1; 64pp; English.
XX
XX The present sequence is the sequence of the DNA polymerase gene from a
CC strain of hepatitis B virus (HBV). It is given in a specification
CC relating to a method for monitoring anti-HBV drug resistance in a patient
CC by genetic detection of any one of mutations L528M, M552V/I and/or
CC V/L/M551 in HBV DNA polymerase in a biological sample from the patient.
CC The method is useful in the field of genetic detection of anti-HBV drug
CC resistance during HBV therapy. The method is rapid, reliable and precise
XX
XX Sequence 297 BP; 63 A; 82 C; 65 G; 87 T; 0 U; 0 Other;
SQ
Query Match 95.4%; Score 65.8; DB 4; Length 297;
Best Local Similarity 97.1%; Pred. No. 1.5e-14;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAACCTACGGAC 60
DB 50 ACGACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAACCTACGGAC 109
QY 61 AGAAACTGC 69
DB 110 GGAAACTGC 118

RESULT 10
ADD44437
ID ADD44437 standard; DNA; 306 BP.
XX
XX ADD44437;
AC
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX RNA virus vector related HBV DNA #1.
DE
XX
XX genetic stability; foreign insert;
XX recombinant single-stranded RNA virus vector; mutagenesis; G/C content;
KW ds.
XX
XX Hepatitis B virus.
OS
XX
XX KR2002066048-A.
PN
XX
XX 14-AUG-2002.
PD
XX
XX 08-FEB-2001; 2001KR-00006229.
PF
XX
XX 08-FEB-2001; 2001KR-00006229.
PR
XX
XX (CREA-) CREAGENE INC.
PA
XX
XX Bae YS, Kim DY, Kim GT, Lee SG;
PI
XX
XX WPI; 2003-145037/14.
DR
XX
XX Improving genetic stability of a foreign insert nucleotide sequence in a
PT recombinant single-stranded RNA virus comprises performing a mutagenesis
PT of the foreign insert to provide even distribution of or to increase G/C
PT

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PT content.
XX Disclosure; SEQ ID NO 17; 24pp; Korean.
XX
XX The invention relates to a novel method for improving genetic stability
XX of a foreign insert nucleotide sequence in a recombinant single-stranded
XX RNA virus vector. The method comprises performing mutagenesis of a
XX foreign insert nucleotide sequence to provide even distribution of G/C
XX content throughout the overall foreign insert nucleotide sequence, and/or
XX to increase G/C content of the foreign insert without causing amino acid
XX substitutions. The method is useful in improving genetic stability of a
XX foreign insert nucleotide sequence in a recombinant RNA virus. This
XX polynucleotide sequence represents a virus DNA sequence relating to the
XX recombinant single-stranded RNA virus vector of the invention.
XX
XX Sequence 306 BP; 75 A; 85 C; 57 G; 89 T; 0 U; 0 Other;
Query Match 95.4%; Score 65.8; DB 9; Length 306;
Best Local Similarity 97.1%; Pred. No. 1.5e-14;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
DB 199 ACAGCTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 258
QY 61 AGAAACTGC 69
DB 259 GGAAACTGC 267
RESULT 11
AAD00819
ID AAD00819 standard; DNA; 426 BP.
AC AAD00819;
XX
XX 15-SEP-2003 (revised)
DT 04-OCT-2000 (first entry)
XX
XX Hepatitis B virus (HBV) 221499/HPBADW3 strain HBSAg encoding DNA.
DE
XX Hepatitis B surface antigen; HBSAg; Hepatitis B virus; HBV; vaccine;
KW immunological profile; reference HBV; HBV polymerase; mutation;
KW screening; treatment; prophylaxis; HBV infection; virucide; hepatotropic;
KW antiinflammatory; ds.
XX
XX Hepatitis B virus; 221499/HPBADW3.
OS
XX WO200028009-A1.
FN
XX 18-MAY-2000.
PD
XX 10-NOV-1999; 99WO-AU0000993.
PF
XX 11-NOV-1998; 98AU-00007060.
PR
XX (NWHE-) NORTH WESTERN HEALTH CARE NETWORK.
FA
XX Locarnini SA, Torresi J, Earnest-Silveira L, Bartholomeusz AI;
PI WPI; 2000-376527/32.
DR
XX Novel variant Hepatitis B virus and viral surface antigens exhibiting
PT altered immunological profile useful for prophylaxis and treatment of
PT Hepatitis B viral infection.
XX
XX Example 3; Fig 3; 70pp; English.
XX The present sequence is the Hepatitis B virus (HBV) DNA of strain
XX 221499/HPBADW3, encoding a portion of the surface antigen (HBSAg). The
XX variant HBSAg comprises of single or multiple amino acid substitution,
XX addition and/or deletion mutations, with an altered immunological
XX profile, relative to an HBSAg from a reference HBV. These variants are

CC less susceptible to vaccines directed to the surface components and
CC arises from selective immune pressure, following anti-HBV chemical
CC therapy, aimed at disrupting HBV polymerase activity or function. Immune
CC pressure may result from natural exposure to HBV or following vaccination
CC with an avirulent or attenuated HBV or with a component of HBV. Variant
CC HBV or HBSAg is useful for screening for an agent and for treatment or
CC prophylaxis of HBV infection. These variants or recombinant polypeptides
CC are also useful in biological compositions capable of inducing a
CC neutralising immune response to the HBV variant. (Updated on 15-SEP-2003
XX to standardise OS field)
XX
XX Sequence 426 BP; 84 A; 112 C; 87 G; 143 T; 0 U; 0 Other;
Query Match 95.4%; Score 65.8; DB 3; Length 426;
Best Local Similarity 97.1%; Pred. No. 1.7e-14;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
DB 118 ACGACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 177
QY 61 AGAAACTGC 69
DB 178 GGAAACTGC 186
RESULT 12
AAD14305
ID AAD14305 standard; DNA; 426 BP.
XX
XX AAD14305;
AC
XX 11-SEP-2003 (revised)
DT 06-NOV-2001 (first entry)
XX
XX Hepatitis B virus (HBV) 221499/HPBADW3 strain HBSAg encoding DNA.
DE
XX Hepatitis B virus; HBV; altered sensitivity; agent; detection;
KW Hepatitis B surface antigen; HBSAg; ss.
XX
XX Hepatitis B virus; 221499/HPBADW3.
OS
XX WO200157244-A1.
PN
XX 09-AUG-2001.
PD
XX 02-FEB-2001; 2001WO-AU0000098.
PF
XX 03-FEB-2000; 2000US-0179948P.
PR
XX (MELB-) MELBOURNE HEALTH.
PA (PENN-) PENN STATE RES FOUND.
XX
XX Delaney W, Locarnini SA, Chen RYM, Bartholomeusz A, Isom H;
PI WPI; 2001-496926/54.
DR
XX Detecting hepatitis B virus variant with altered sensitivity to agent,
PT comprises infecting genetic construct containing replication competent
PT genome to cells, contacting cells with agent and detecting replication of
PT variant.
XX
XX Example 3; Fig 3; 110pp; English.
XX The invention relates to a method of detecting variant hepatitis B virus
XX (HBV) which exhibits altered sensitivity to agents. The method involves
XX infecting a genetic construct containing a replication competent amount
XX of the genome from variant HBV contained in or fused to a baculovirus
XX genome; contacting cells with the agent to be tested; culturing cells
XX under conditions sufficient for the variant HBV to replicate, express
XX genetic sequences, and/or assemble, and/or release viral particles; and
XX determining replication of variant HBV using viral-component-detection
XX means. The method is useful for detecting variant HBV which exhibits

CC altered sensitivity to agents. The present sequence is the HBV DNA of
CC strain 221499/HBADM3, encoding a portion of the surface antigen (HBSAg).
CC (Updated on 11-SEP-2003 to standardise OS field)

CC Sequence 426 BP; 84 A; 112 C; 87 G; 143 T; 0 U; 0 Other;

Query Match 95.4%; Score 65.8; DB 4; Length 426;
Best Local Similarity 97.1%; Pred. No. 1.7e-14;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTCTGTACAAAACCTACGGAC 60
Db 118 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTCTGTACAAAACCTACGGAC 177

QY 61 AGAAACTGC 69
Db 178 GGAACACTGC 186

RESULT 13

AAAT58385
ID AAT58385 standard; DNA; 477 BP.

XX AAT58385;

DT 04-AUG-1997 (first entry)

XX Hepatitis B virus target sequence (map positions 236-712).

XX detection; primer; set; amplicon; threshold concentration; probe;
KW ligase chain reaction; LCR; bacteria; virus; HIV; PCR; amplify;
KW Chlamydia trachomatis; ds.

XX Hepatitis B virus.

XX WO9636736-A2.

XX 21-NOV-1996.

XX 17-MAY-1996; 96WO-US007138.

XX 19-MAY-1995; 95US-00444615.

XX (ABBO) ABBOTT LAB.

XX Solomon NA, Bouma SR;

XX WPI; 1997-012104/01.

XX Detection of target nucleic acid sequences - using different primer sets
XX capable of producing detectable amplicons at different threshold concns.

XX Example 2; Page 29; 46pp; English.

XX Determining approximate amounts of target nucleic acid sequences in a
CC sample comprises contacting the sample with an amplification reaction
CC mixture comprising 2 (different) primer sets which react with 2
CC (different) sub-target regions of the target sequence, the sets being
CC selected such that they are capable of producing a detectable amplicon
CC only at or above a certain threshold concn. of the target sequence, the
CC threshold concns. being different for each primer set. The reaction
CC mixture is subjected to amplification conditions sufficient to produce a
CC detectable amplicon from at least one of the primer sets when the test
CC sample contains a concn. of target sequence which is at or above the
CC threshold concn. at which the primer set is capable of producing a
CC detectable amplicon. The reaction mixture is analysed to determine
CC whether an amplicon was produced in the reaction mixture from at least
CC one primer set so as to determine whether the test sample contains a
CC concn. of target sequence at or above the threshold concn. corresponding
CC to at least one primer. The method can be used for the detection of
CC targets such as bacteria or viruses, e.g. HIV or Chlamydia trachomatis.
CC The method can provide for the detection of a relative or approximate
CC amt. of a target sequence in a test sample without requiring extensive

CC sample manipulation or preparation. Simultaneous PCR of two separate sub-
CC target regions of an Hepatitis B Virus (HBV) target sequence was
CC performed using two primer sets which have widely differing
CC sensitivities. The present sequence comprises the first sub-target
CC sequence corresponding to map positions 236-712 of HBV. AAT58387-88
CC comprise the primer set for this target sequence

SQ Sequence 477 BP; 96 A; 135 C; 96 G; 150 T; 0 U; 0 Other;

Query Match 95.4%; Score 65.8; DB 2; Length 477;
Best Local Similarity 97.1%; Pred. No. 1.7e-14;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTCTGTACAAAACCTACGGAC 60

Db 292 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTCTGTACAAAACCTACGGAT 351

QY 61 AGAAACTGC 69

Db 352 GGAACACTGC 360

RESULT 14

AAQ75318
ID AAQ75318 standard; DNA; 684 BP.

XX AAQ75318;

DT 25-MAR-2003 (revised)

DT 22-SEP-1995 (first entry)

XX Mutant Hepatitis B virus nucleic acid sequence.

XX Hepatitis B virus; HBV; mutant; detection; surface antigen; HBSAg;
KW detection; vaccine; diagnostic; prognosis; therapy; ss.

XX Hepatitis B virus.

XX Key Location/Qualifiers
FT misc_difference 185..187

FT /tag= a

FT /transl_except= AAC encodes Threonine.

FT misc_difference 289..291

FT /tag= b

FT /transl_except= CCT encodes Leucine.

FT insertion_seq 367..372

FT /tag= c

XX WO9426904-A1.

XX 24-NOV-1994.

XX 09-MAY-1994; 94WO-US005090.

XX 07-MAY-1993; 93US-00059031.

XX (ABBO) ABBOTT LAB.

XX (UNIU) UNIV GLASGOW.

XX Carman W, Decker RH, Wallace L, Mims LT, Solomon LR;
XX WPI; 1995-006799/01.

XX P-PSDB; AAR67368.

XX New mutant hepatitis B virus polynucleotide - used to develop prods. for
XX diagnosis, prognosis, therapy and studies involving hepatitis B
XX infection.

XX Example 2; Page 48-49; 59pp; English.

XX The mutant hepatitis B virus (HBV) polynucleotide comprises an insertion
XX of six nucleotides at position 366 of the HBV surface antigen (HBSAg)
XX gene. The polynucleotide can be used for detection of mutant HBV and for

CC the production of mutant polypeptides which can be used in vaccines for
CC the treatment of infection. Antibodies against such polypeptides can be
CC used for detecting the mutant HBV antigen. (Updated on 25-MAR-2003 to
CC correct PN field.)

XX SQ Sequence 684 BP; 140 A; 189 C; 142 G; 213 T; 0 U; 0 Other;
Query Match 95.4%; Score 65.8; DB 2; Length 684;
Best Local Similarity 97.1%; Pred. No. 1.9e-14; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 2

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 379 ACGACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 438
QY 61 AGAAACTGC 69
Db 439 AGAAACTGC 447

RESULT 15
AAD00829
ID AAD00829 standard; DNA; 426 BP.
XX AC AAD00829;
XX DT 15-SEP-2003 (revised)
XX DT 04-OCT-2000 (first entry)
XX DE Hepatitis B virus (HBV) 229417/HPBADW1 strain HbsAg encoding DNA.
XX KW Hepatitis B surface antigen; HbsAg; Hepatitis B virus; HBV; vaccine;
XX KW immunological profile; reference HBV; HBV polymerase; mutation;
XX KW screening; treatment; prophylaxis; HBV infection; virucide; hepatotropic;
XX KW antiinflammatory; ds.
XX OS Hepatitis B virus; 229417/HPBADW1.
XX PN WO200028009-A1.
XX PD 18-MAY-2000.
XX PF 10-NOV-1999; 99WO-AU000993.
XX PR 11-NOV-1998; 98AU-00007060.
XX PA (NWHE-) NORTH WESTERN HEALTH CARE NETWORK.
XX PI Locarnini SA, Torresi J, Earnest-Silveira L, Bartholomeusz AI;
XX WPI; 2000-376527/32.
XX Novel variant Hepatitis B virus and viral surface antigens exhibiting
XX altered immunological profile useful for prophylaxis and treatment of
XX Hepatitis B viral infection.
XX Example 3; Fig 3; 70pp; English.
XX The present sequence is the Hepatitis B virus (HBV) DNA of strain
XX 229417/HPBADW1, encoding a portion of the surface antigen (HbsAg). The
XX variant HbsAg comprises of single or multiple amino acid substitution,
XX addition and/or deletion mutations, with an altered immunological
XX profile, relative to an HbsAg from a reference HBV. These variants are
XX less susceptible to vaccines directed to the surface components and
XX arises from selective immune pressure, following anti-HBV chemical
XX therapy, aimed at disrupting HBV polymerase activity or function. Immune
XX pressure may result from natural exposure to HBV or following vaccination
XX with an avirulent or attenuated HBV or with a component of HBV. Variant
XX HBV or HbsAg is useful for screening for an agent and for treatment or
XX prophylaxis of HBV infection. These variants or recombinant polypeptides
XX are also useful in biological compositions capable of inducing a
XX neutralising immune response to the HBV variant. (Updated on 15-SEP-2003
XX to standardise OS field)

XX SQ Sequence 426 BP; 84 A; 110 C; 88 G; 144 T; 0 U; 0 Other;
Query Match 93.0%; Score 64.2; DB 3; Length 426;
Best Local Similarity 95.7%; Pred. No. 6.6e-14; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 3

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 118 ACAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTATGGAT 177
QY 61 AGAAACTGC 69
Db 178 GGAAGACTGC 186

Search completed: July 26, 2004, 16:43:27
Job time : 201 secs


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Db          439 GGAAGCTGC 447
|||||
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/697,404
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/444,615A
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul D. Yasger
REGISTRATION NUMBER: 37,477
REFERENCE/DOCKET NUMBER: 5692.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-2341
TELEFAX: 708/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA (HBV)
US-08-697-404-11

Query Match          95.4%; Score 65.8; DB 2; Length 477;
Best Local Similarity 97.1%; Pred. No. 4.4e-16;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 292 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
QY 61 AGAAACTGC 69
Db 352 GGAAGCTGC 360

RESULT 4
US-08-500-914A-7
Sequence 7, Application US/08500914A
Patent No. 5856084
GENERAL INFORMATION:
APPLICANT: KARAYIANNIS, PETER
APPLICANT: THOMAS, HOWARD C.
TITLE OF INVENTION: HEPATITIS B VACCINE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/500,914A
FILING DATE: 28-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MITCHARD, LEONARD C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 1208-17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 690 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-500-914A-8

Query Match          97.7%; Score 67.4; DB 2; Length 690;
Best Local Similarity 98.6%; Pred. No. 1.2e-16;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 382 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 441
QY 61 AGAAACTGC 69
Db 442 GGAAGCTGC 450

RESULT 3
US-08-697-404-11
Sequence 11, Application US/08697404
Patent No. 5858732
GENERAL INFORMATION:
APPLICANT: N. A. Solomon
APPLICANT: S. R. Bounda
TITLE OF INVENTION: WIDE DYNAMIC RANGE NUCLEIC ACID
TITLE OF INVENTION: DETECTION USING AN AGGREGATE
TITLE OF INVENTION: PRIMER SERIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
```

REFERENCE/DOCKET NUMBER: 1208-17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 681 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-500-914A-7

Query Match 95.4%; Score 65.8; DB 2; Length 681;
Best Local Similarity 97.1%; Pred. No. 5e-16; 2; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 373 ACAGCTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 432

QY 61 AGAAACTGC 69
Db 433 GGAAGCTGC 441

RESULT 5
US-08-500-914A-9
Sequence 9, Application US/08500914A
Patent No. 5856084
GENERAL INFORMATION:
APPLICANT: KARAYIANNIS, PETER
APPLICANT: THOMAS, HOWARD C.
TITLE OF INVENTION: HEPATITIS B VACCINE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,914A
FILING DATE: 28-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MITCHARD, LEONARD C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 1208-17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 681 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-500-914A-9

Query Match 95.4%; Score 65.8; DB 2; Length 681;
Best Local Similarity 97.1%; Pred. No. 5e-16; 2; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 373 ACAGCTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 432

Db 373 ACAGCTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 432

QY 61 AGAAACTGC 69
Db 433 GGAAGCTGC 441

RESULT 6
US-08-447-591-1
Sequence 1, Application US/08447591
Patent No. 5591440
GENERAL INFORMATION:
APPLICANT: CARMAN, WILLIAM
APPLICANT: DECKER, RICHARD H
APPLICANT: WALLACE, LESLEY
APPLICANT: MIMMS, LARRY T
APPLICANT: SOLOMON, LARRY R
TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,591
FILING DATE: 23-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,031
FILING DATE: 07-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5347 US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..684
US-08-447-591-1

Query Match 95.4%; Score 65.8; DB 1; Length 684;
Best Local Similarity 97.1%; Pred. No. 5e-16; 0; Mismatches 2; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 379 ACAGCTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 438

QY 61 AGAAACTGC 69
Db 439 AGAAACTGC 447

RESULT 7
US-08-450-943-1
Sequence 1, Application US/08450943

Patent No. 5593825
GENERAL INFORMATION:
APPLICANT: CARMAN, WILLIAM
APPLICANT: DECKER, RICHARD H
APPLICANT: WALLIS, LESLEY
APPLICANT: MIMMS, LARRY T
APPLICANT: SOLOMON, LARRY R
TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR
DETECTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,943
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5347.US.01
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..684
US-08-450-943-1

Query Match 95.4%; Score 65.8; DB 1; Length 684;
Best Local Similarity 97.1%; Pred. No. 5e-16; 2; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 0; Gaps 0;
QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTTCCTCATGTTGCTGTACAAAACCTACGGAC 60
DB 379 ACGACTCCTGCTCAAGGAACCTCTATGTTTCCTCATGTTGCTGTACAAAACCTACGGAC 438
QY 61 AGAAACTGC 69
DB 439 AGAAACTGC 447

RESULT 8
US-08-059-031-1
Sequence 1, Application US/08059031
Patent No. 5595739
GENERAL INFORMATION:
APPLICANT: CARMAN, WILLIAM
APPLICANT: DECKER, RICHARD H
APPLICANT: WALLIS, LESLEY
APPLICANT: MIMMS, LARRY T
APPLICANT: SOLOMON, LARRY R
TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD

CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/059,031
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5347.US.01
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..684
US-08-059-031-1

Query Match 95.4%; Score 65.8; DB 1; Length 684;
Best Local Similarity 97.1%; Pred. No. 5e-16; 2; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 0; Gaps 0;
QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTTCCTCATGTTGCTGTACAAAACCTACGGAC 60
DB 379 ACGACTCCTGCTCAAGGAACCTCTATGTTTCCTCATGTTGCTGTACAAAACCTACGGAC 438
QY 61 AGAAACTGC 69
DB 439 AGAAACTGC 447

RESULT 9
US-08-450-942-1
Sequence 1, Application US/08450942
Patent No. 5525512
GENERAL INFORMATION:
APPLICANT: CARMAN, WILLIAM
APPLICANT: DECKER, RICHARD H
APPLICANT: WALLIS, LESLEY
APPLICANT: MIMMS, LARRY T
APPLICANT: SOLOMON, LARRY R
TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,942
FILING DATE:
CLASSIFICATION: 435

```
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5347.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..684
US-08-450-942-1

Query Match 95.4%; Score 65.8; DB 2; Length 684;
Best Local Similarity 97.1%; Pred. No. 5e-16;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 379 ACGACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 438

QY 61 AGAAACTGC 69
Db 439 AGAAACTGC 447

RESULT 10
PCT-US94-05090-1
Sequence 1. Application PC/TUS9405090
GENERAL INFORMATION:
APPLICANT: CARMAN, WILLIAM
APPLICANT: DECKER, RICHARD H
APPLICANT: WALLACE, LESLEY
APPLICANT: MINNS, LARRY T
APPLICANT: SOLOMON, LARRY R
TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05090
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5347.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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FEATURE:
NAME/KEY: CDS
LOCATION: 1..684
PCT-US94-05090-1

Query Match 95.4%; Score 65.8; DB 5; Length 684;
Best Local Similarity 97.1%; Pred. No. 5e-16;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 379 ACGACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 438

QY 61 AGAAACTGC 69
Db 439 AGAAACTGC 447

RESULT 11
US-09-471-573A-1
Sequence 1. Application US/09471573A
Patent No. 6551820
GENERAL INFORMATION:
APPLICANT: Mason, Hugh
APPLICANT: Thanavala, Yasmin
TITLE OF INVENTION: Expression of Immunogenic Hepatitis B Surface Antigens In Transgene
FILE REFERENCE: 3121/1080
CURRENT APPLICATION NUMBER: US/09/471,573A
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,827
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 681
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hepatitis B surface antigen
NAME/KEY: misc feature
OTHER INFORMATION: Hepatitis B surface antigen
US-09-471-573A-1

Query Match 88.4%; Score 61; DB 4; Length 681;
Best Local Similarity 92.8%; Pred. No. 3.6e-14;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 373 ACGATTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 432

QY 61 AGAAACTGC 69
Db 433 AGAAACTGC 441

RESULT 12
US-08-378-011A-4
Sequence 4. Application US/08378011A
Patent No. 5693497
GENERAL INFORMATION:
APPLICANT: TAKAMIZAWA, Akihisa
APPLICANT: FUJITA, Hiroyuki
APPLICANT: MANABE, Sadao
APPLICANT: KATO, Masahiko
APPLICANT: OSAME, Juichiro
APPLICANT: YOSHIDA, Iwao
APPLICANT: KONOBE, Takeo
APPLICANT: TAKAKU, Keisuke
TITLE OF INVENTION: HEPATITIS B VIRUS ANTIGEN AND A PROCESS FOR
PRODUCING SAME
NUMBER OF SEQUENCES: 4
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Armstrong, Westernman, Hattori, McLeLeland &
;; ADDRESSEE: Naughton
;; STREET: 1725 K St. N.W. Suite 1000
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20006
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
;; SOFTWARE: ASCII, generated using Word Perfect, version 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/378,011A
;; FILING DATE: 25-JAN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 61-143412
;; FILING DATE: 18-JUN-1986
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/061,518
;; FILING DATE: 15-JUN-1987
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/902,494
;; FILING DATE: 23-JUN-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stevens-Smith, Theresa M.
;; REGISTRATION NUMBER: 36,281
;; REFERENCE/DOCKET NUMBER: 870602B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 659-2930
;; TELEFAX: (202) 887-0357
;; TELEX: 440142
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 817 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna from genomic RNA
US-08-378-011A-4

Query Match 88.4%; Score 61; DB 1; Length 817;
Best Local Similarity 92.8%; Pred. No. 3.8e-14;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
DB 512 ACGATTCTGCTCAAGGAACCTCTATGTTCCCTCTTGTGCTGTACAAAACCTTCGGAC 571
QY 61 AGAAACTGC 69
DB 572 GGAACACTGC 580

RESULT 13
US-08-378-011A-2
; Sequence 2, Application US/08378011A
; Patent No. 5693497
; GENERAL INFORMATION:
; APPLICANT: TAKAMIZAWA, Akihisa
; APPLICANT: FUJITA, Hiroyuki
; APPLICANT: MANABE, Sadao
; APPLICANT: KATO, Masahiko
; APPLICANT: OSAME, Juichiro
; APPLICANT: YOSHIDA, Iwao
; APPLICANT: KONOBE, Takeo
; APPLICANT: TAKAKU, Keisuke
; TITLE OF INVENTION: HEPATITIS B VIRUS ANTIGEN AND A PROCESS FOR
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Armstrong, Westernman, Hattori, McLeLeland &
;; ADDRESSEE: Naughton
;; STREET: 1725 K St. N.W. Suite 1000
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20006
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
;; SOFTWARE: ASCII, generated using Word Perfect, version 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/378,011A
;; FILING DATE: 25-JAN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 61-143412
;; FILING DATE: 18-JUN-1986
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/061,518
;; FILING DATE: 15-JUN-1987
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/902,494
;; FILING DATE: 23-JUN-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stevens-Smith, Theresa M.
;; REGISTRATION NUMBER: 36,281
;; REFERENCE/DOCKET NUMBER: 870602B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 659-2930
;; TELEFAX: (202) 887-0357
;; TELEX: 440142
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 845 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna from genomic RNA
US-08-378-011A-2

Query Match 88.4%; Score 61; DB 1; Length 845;
Best Local Similarity 92.8%; Pred. No. 3.9e-14;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
DB 540 ACGATTCTGCTCAAGGAACCTCTATGTTCCCTCTTGTGCTGTACAAAACCTTCGGAC 599
QY 61 AGAAACTGC 69
DB 600 GGAACACTGC 608

RESULT 14
5164485-1
; Patent No. 5164485
; APPLICANT: FUJISAWA, YUKIO; ITOH, YASUAKI; NISHIMURA, OSAMU
; FUJII, TOMOKO
; TITLE OF INVENTION: MODIFIED HEPATITIS B VIRUS SURFACE
; ANTIGEN P31 AND PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/547,948
; FILING DATE: 03-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 898,425
; FILING DATE: 20-AUG-1986
; SEQ ID NO: 1
; LENGTH: 846
5164485-1

Query Match 88.4%; Score 61; DB 6; Length 846;
Best Local Similarity 92.8%; Pred. No. 3.9e-14;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
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Db 538 ACGATTCTGCTCAAGAACCTCTATGTTCCCTCTGTTGCTGTACAAAACCTTCGGAC 597
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QY 61 AGAAACTGC 69
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Db 598 GGAACCTGC 606
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RESULT 15
US-08-854-531-5
; Sequence 5, Application US/08854531
; Patent No. 6025341
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack
; APPLICANT: Tokushige, Katsutoshi
; APPLICANT: Wakita, Takaji
; TITLE OF INVENTION: CHIMERIC HEPATITIS B/HEPATITIS C VIRUS VACCINE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6025341ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,531
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: APOL-0214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-854-531-5

Query Match 88.4%; Score 61; DB 3; Length 1200;
Best Local Similarity 92.8%; Pred. No. 4.4e-14;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
|||
Db 895 ACGATTCTGCTCAAGAACCTCTATGTTCCCTCTGTTGCTGTACAAAACCTTCGGAC 954
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QY 61 AGAAACTGC 69
|||||

Db 955 GGAACCTGC 963
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Search completed: July 26, 2004, 17:29:04
Job time : 53 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 17:05:50 ; Search time 229 Seconds
(without alignments)
1472.894 Million cell updates/sec

Title: US-09-719-533A-1_COPY_527_595
Perfect score: 69
Sequence: 1 ACAACTCTGCTCAGGAC.....AACCTACGACAGAACTGC 69

Scoring table: IDENTIFY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3216467 seqs, 2444149694 residues
Total number of hits satisfying chosen parameters: 6432934

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications NA.*
- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
 - 3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
 - 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
 - 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
 - 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
 - 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
 - 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
 - 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
 - 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
 - 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
 - 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
 - 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
 - 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
 - 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
 - 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
 - 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
 - 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
 - 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65.8	95.4	306	15	US-10-071-867-19
2	65.8	95.4	425	10	US-09-781-891D-10
3	65.8	95.4	3215	13	US-10-453-792-284
4	65.8	95.4	3215	13	US-10-453-792-285
5	65.8	95.4	3215	13	US-10-453-792-287
6	64.2	93.0	426	10	US-09-781-891D-20
7	64.2	93.0	3215	13	US-10-453-792-286
8	62.6	90.7	3215	13	US-10-453-792-299
9	62.6	90.7	3215	13	US-10-453-792-300
10	61	88.4	426	10	US-09-781-891D-16
11	61	88.4	426	10	US-09-781-891D-17
12	61	88.4	681	17	US-10-335-774-1
13	61	88.4	1203	13	US-10-411-037-45
14	61	88.4	1203	13	US-10-411-026-45

15	61	88.4	1203	17	US-10-410-962-45	Sequence 45, Appl
16	61	88.4	1203	17	US-10-411-043-45	Sequence 45, Appl
17	61	88.4	1203	17	US-10-410-930-45	Sequence 45, Appl
18	61	88.4	1203	17	US-10-410-997-45	Sequence 45, Appl
19	61	88.4	1203	17	US-10-411-012-45	Sequence 45, Appl
20	61	88.4	1203	17	US-10-287-994-45	Sequence 3, Appl
21	61	88.4	1286	15	US-10-132-829-3	Sequence 3, Appl
22	61	88.4	1286	15	US-10-136-819-1	Sequence 1, Appl
23	61	88.4	1286	15	US-10-133-907-3	Sequence 3, Appl
24	61	88.4	3188	13	US-10-453-792-288	Sequence 293, App
25	61	88.4	3213	13	US-10-453-792-289	Sequence 288, App
26	61	88.4	3213	13	US-10-453-792-289	Sequence 289, App
27	61	88.4	3214	13	US-10-453-792-294	Sequence 294, App
28	61	88.4	3215	13	US-10-453-792-290	Sequence 290, App
29	61	88.4	3215	13	US-10-453-792-292	Sequence 292, App
30	61	88.4	3215	13	US-10-453-792-296	Sequence 296, App
31	61	88.4	3215	13	US-10-453-792-297	Sequence 297, App
32	61	88.4	3215	13	US-10-453-792-297	Sequence 11, Appl
33	61	88.4	5130	9	US-09-897-006-9	Sequence 9, Appl
34	61	88.4	5130	10	US-09-897-511A-9	Sequence 9, Appl
35	61	88.4	5130	13	US-10-397-079-9	Sequence 4, Appl
36	59.4	86.1	182	9	US-09-821-877-4	Sequence 9, Appl
37	59.4	86.1	426	10	US-09-781-891D-9	Sequence 11, Appl
38	59.4	86.1	426	10	US-09-781-891D-11	Sequence 15, Appl
39	59.4	86.1	426	10	US-09-781-891D-15	Sequence 17, Appl
40	59.4	86.1	550	15	US-10-260-451-17	Sequence 19, Appl
41	59.4	86.1	550	15	US-10-260-451-19	Sequence 27, Appl
42	59.4	86.1	585	16	US-10-394-896-27	Sequence 3, Appl
43	59.4	86.1	681	9	US-09-821-877-3	Sequence 6, Appl
44	59.4	86.1	690	9	US-09-821-877-6	Sequence 7, Appl
45	59.4	86.1	690	9	US-09-821-877-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-10-071-867-19
; Sequence 19, Application US/10071867
; Publication No. US20030166267A1
; GENERAL INFORMATION:
; APPLICANT: CreaGene Inc.
; TITLE OF INVENTION: METHOD FOR IMPROVING GENETIC STABILITY OF FOREIGN INSERT
; FILE REFERENCE: CreaGene-USA-1
; CURRENT APPLICATION NUMBER: US/10/071.867
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: KR 2001-6229
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 19
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBVCs
US-10-071-867-19

Query Match 95.4%; Score 65.8; DB 15; Length 306;
Best Local Similarity 97.1%; Pred. No. 2.1e-15;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ACAACTCTGCTCAGGACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
DB 199 ACAGTCTCTGCTCAGGACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 258
QY 61 AGAAACTGC 69
DB 259 GGAAACTGC 267

RESULT 2

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US-09-781-891D-10
; Sequence 10, Application US/09781891D
; Publication No. US20030096222A1
; GENERAL INFORMATION:
; APPLICANT: Delaney, William IV
; APPLICANT: Locarnini, Stephen Alister
; APPLICANT: Chen, Robert Yung Ming
; APPLICANT: Bartholomewsz, Angeline
; APPLICANT: Isom, Harriet
; TITLE OF INVENTION: An assay
; FILE REFERENCE: 2378750/ETH
; CURRENT APPLICATION NUMBER: US/09/781,891D
; CURRENT FILING DATE: 2001-02-02
; PRIOR FILING DATE: 60/179,948
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 10
; LENGTH: 425
; TYPE: DNA
; ORGANISM: HBV
US-09-781-891D-10

Query Match          95.4%; Score 65.8; DB 10; Length 425;
Best Local Similarity 97.1%; Pred. No. 2.3e-15;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAAATCTCTCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 118 ACGACTCCTCTCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 177

QY 61 AGAAACTGC 69
Db 178 GGAACACTGC 186

RESULT 3
US-10-453-792-284
; Sequence 284, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 285:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
;
US-09-719-533a-1_copy_527_595.rnpb

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 284:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 284:
US-10-453-792-284

Query Match          95.4%; Score 65.8; DB 13; Length 3215;
Best Local Similarity 97.1%; Pred. No. 4.6e-15;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAAATCTCTCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 529 ACGACTCCTCTCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 588

QY 61 AGAAACTGC 69
Db 589 GGAACACTGC 597

RESULT 4
US-10-453-792-285
; Sequence 285, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 285:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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Best Local Similarity 97.1%; Pred. No. 4.6e-15;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ACAAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 529 ACAAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAT 588
QY 61 AGAAACTGC 69
Db 589 GGAAACTGC 597
RESULT 6
US-09-781-891D-20
; Sequence 20, Application US/09781891D
; Publication No. US2003009622A1
; GENERAL INFORMATION:
; APPLICANT: Delaney, William IV
; APPLICANT: Locarnini, Stephen Alister
; APPLICANT: Chen, Robert Yung Ming
; APPLICANT: Bartholomeusz, Angeline
; APPLICANT: Isom, Harriet
; TITLE OF INVENTION: An assay
; FILE REFERENCE: 2378750/EJH
; CURRENT APPLICATION NUMBER: US/09/781,891D
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,948
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 20
; LENGTH: 426
; TYPE: DNA
; ORGANISM: HBV
US-09-781-891D-20
Query Match 93.0%; Score 64.2; DB 10; Length 426;
Best Local Similarity 95.7%; Pred. No. 9.9e-15;
Matches 66; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ACAAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 118 ACAAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTATGGAT 177
QY 61 AGAAACTGC 69
Db 178 GGAAACTGC 186
RESULT 7
US-10-453-792-286
; Sequence 286, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-Apr-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 287:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 287:
US-10-453-792-287
Query Match 95.4%; Score 65.8; DB 13; Length 3215;

TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 285:
US-10-453-792-285
Query Match 95.4%; Score 65.8; DB 13; Length 3215;
Best Local Similarity 97.1%; Pred. No. 4.6e-15;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ACAAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 529 ACAAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 588
QY 61 AGAAACTGC 69
Db 589 GGAAACTGC 597
RESULT 5
US-10-453-792-287
; Sequence 287, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-Apr-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 287:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 287:
US-10-453-792-287
Query Match 95.4%; Score 65.8; DB 13; Length 3215;

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/ FILING DATE: 04-Jun-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/155,885A
/ FILING DATE: 08-Oct-1998
/ APPLICATION NUMBER: PCT/EP97/02002
/ FILING DATE: 21-Apr-1997
/ APPLICATION NUMBER: EP 96870053.4
/ FILING DATE: 19-Apr-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: SADOFF, B.J.
/ REGISTRATION NUMBER: 36,663
/ REFERENCE/DOCKET NUMBER: 2551-5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 816-4000
/ TELEFAX: (703) 816-4100
/ INFORMATION FOR SEQ ID NO: 286:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3215 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ SEQUENCE DESCRIPTION: SEQ ID NO: 286:
US-10-453-792-286

Query Match 93.08; Score 64.2; DB 13; Length 3215;
Best Local Similarity 95.7%; Pred. No. 1.9e-14;
Matches 66; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGACAAAACCTACGGAC 60
Db 529 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGACAAAACCTATGGAT 588
QY 61 AGAAACTGC 69
Db 589 GGAACCTGC 597

RESULT 8
US-10-453-792-299
/ Sequence 299, Application US/10453792
/ Publication No. US20040029110A1
/ GENERAL INFORMATION:
/ APPLICANT: STUYVER, LIEVEN
/ ROSSAU, RUDI
/ MAERTENS, GEERT
/ TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
/ NUMBER OF SEQUENCES: 313
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: NIXON & VANDERHUYE P.C.
/ STREET: 1100 NORTH GLEBE ROAD
/ CITY: ARLINGTON
/ STATE: VIRGINIA
/ COUNTRY: U.S.A.
/ ZIP: 22201-4714
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/453,792
/ FILING DATE: 04-Jun-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/155,885A
/ FILING DATE: 08-Oct-1998
/ APPLICATION NUMBER: PCT/EP97/02002
/ FILING DATE: 21-Apr-1997
/ APPLICATION NUMBER: EP 96870053.4
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/ FILING DATE: 19-Apr-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: SADOFF, B.J.
/ REGISTRATION NUMBER: 36,663
/ REFERENCE/DOCKET NUMBER: 2551-5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 816-4000
/ TELEFAX: (703) 816-4100
/ INFORMATION FOR SEQ ID NO: 299:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3215 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ SEQUENCE DESCRIPTION: SEQ ID NO: 299:
US-10-453-792-299

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Best Local Similarity 94.2%; Pred. No. 8.2e-14;
Matches 65; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGACAAAACCTACGGAC 60
Db 529 ACGATTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGACAAAACCTTCGGAC 588
QY 61 AGAAACTGC 69
Db 589 GGAACCTGC 597

RESULT 9
US-10-453-792-300
/ Sequence 300, Application US/10453792
/ Publication No. US20040029110A1
/ GENERAL INFORMATION:
/ APPLICANT: STUYVER, LIEVEN
/ ROSSAU, RUDI
/ MAERTENS, GEERT
/ TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
/ NUMBER OF SEQUENCES: 313
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: NIXON & VANDERHUYE P.C.
/ STREET: 1100 NORTH GLEBE ROAD
/ CITY: ARLINGTON
/ STATE: VIRGINIA
/ COUNTRY: U.S.A.
/ ZIP: 22201-4714
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/453,792
/ FILING DATE: 04-Jun-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/155,885A
/ FILING DATE: 08-Oct-1998
/ APPLICATION NUMBER: PCT/EP97/02002
/ FILING DATE: 21-Apr-1997
/ APPLICATION NUMBER: EP 96870053.4
/ FILING DATE: 19-Apr-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: SADOFF, B.J.
/ REGISTRATION NUMBER: 36,663
/ REFERENCE/DOCKET NUMBER: 2551-5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 816-4000
/ TELEFAX: (703) 816-4100
```

```
; INFORMATION FOR SEQ ID NO: 300:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 3215 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 300:
US-10-453-792-300

Query Match      90.7%; Score 62.6; DB 13; Length 3215;
Best Local Similarity 94.2%; Pred. No. 8.2e-14;
Matches 65; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 60
Db 529 ACGATTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 588

QY 61 AGAAACTGC 69
Db 589 GGAACCTGC 597

RESULT 10
US-09-781-891D-16
; Sequence 16, Application US/09781891D
; Publication No. US20030096222A1
; GENERAL INFORMATION:
; APPLICANT: Delaney, William IV
; APPLICANT: Locarnini, Stephen Alister
; APPLICANT: Chen, Robert Yung Ming
; APPLICANT: Bartholomeusz, Angeline
; APPLICANT: Isom, Harriet
; TITLE OF INVENTION: An assay
; FILE REFERENCE: 2378750/EJH
; CURRENT APPLICATION NUMBER: US/09/781,891D
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,948
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 16
; LENGTH: 426
; TYPE: DNA
; ORGANISM: HBV
US-09-781-891D-16

Query Match      88.4%; Score 61; DB 10; Length 426;
Best Local Similarity 92.8%; Pred. No. 1.7e-13;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 61 AGAAACTGC 69
Db 178 GGAACCTGC 186

RESULT 11
US-09-781-891D-17
; Sequence 17, Application US/09781891D
; Publication No. US20030096222A1
; GENERAL INFORMATION:
; APPLICANT: Delaney, William IV
; APPLICANT: Locarnini, Stephen Alister
; APPLICANT: Chen, Robert Yung Ming
; APPLICANT: Bartholomeusz, Angeline
; APPLICANT: Isom, Harriet
; TITLE OF INVENTION: An assay
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; FILE REFERENCE: 2378750/EJH
; CURRENT APPLICATION NUMBER: US/09/781,891D
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,948
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 17
; LENGTH: 426
; TYPE: DNA
; ORGANISM: HBV
US-09-781-891D-17

Query Match      88.4%; Score 61; DB 10; Length 426;
Best Local Similarity 92.8%; Pred. No. 1.7e-13;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 60
Db 118 ACGATTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 177

QY 61 AGAAACTGC 69
Db 178 GGAACCTGC 186

RESULT 12
US-10-335-774-1
; Sequence 1, Application US/10335774
; Publication No. US20040086530A1
; GENERAL INFORMATION:
; APPLICANT: Mason, Hugh S.
; APPLICANT: Thanavala, Yasmin
; TITLE OF INVENTION: Expression of Immunogenic Hepatitis B Surface Antigens In Transgenic Plants
; FILE REFERENCE: 3121/1083
; CURRENT APPLICATION NUMBER: US/10/335,774
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 60/113,827
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 09/471,573
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Hepatitis B virus
; NAME/KEY: misc feature
; OTHER INFORMATION: Hepatitis B surface antigen
US-10-335-774-1

Query Match      88.4%; Score 61; DB 17; Length 681;
Best Local Similarity 92.8%; Pred. No. 2e-13;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 373 ACGATTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 432

QY 61 AGAAACTGC 69
Db 433 GGAACCTGC 441

RESULT 13
US-10-411-037-45
; Sequence 45, Application US/10411037
; Publication No. US2004004346A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePrees, Shawn
```

APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bove, Caryn
TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
FILE REFERENCE: 040853-01-5082
CURRENT APPLICATION NUMBER: US/10/411,037
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 45
LENGTH: 1203
TYPE: DNA
ORGANISM: Hepatitis B virus
US-10-411-037-45

Query Match 88.4%; Score 61; DB 13; Length 1203;
Best Local Similarity 92.8%; Pred. No. 2.5e-13;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACACTCTCTCTCAAGAACCTTATGTTTCCCTCATGTTGCTGTACAAACCTACGGAC 60
Db 895 ACGATTCCTCTCAAGAACCTTATGTTTCCCTCATGTTGCTGTACAAACCTACGGAC 954

QY 61 AGAAACTGC 69
Db 955 GGAAACTGC 963

RESULT 14
US-10-411-026-45
Sequence 45, Application US/10411026
Publication No. US20040063911A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
FILE REFERENCE: 040853-01-5053
CURRENT APPLICATION NUMBER: US/10/411,026
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 45
LENGTH: 1203
TYPE: DNA
ORGANISM: Hepatitis B virus
US-10-411-026-45

Query Match 88.4%; Score 61; DB 13; Length 1203;
Best Local Similarity 92.8%; Pred. No. 2.5e-13;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACACTCTCTCTCAAGAACCTTATGTTTCCCTCATGTTGCTGTACAAACCTACGGAC 60
Db 895 ACGATTCCTCTCAAGAACCTTATGTTTCCCTCATGTTGCTGTACAAACCTACGGAC 954

QY 61 AGAAACTGC 69
Db 955 GGAAACTGC 963

RESULT 15
US-10-410-962-45
Sequence 45, Application US/10410962
Publication No. US20040077836A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bove, Caryn
TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
FILE REFERENCE: 040853-01-5054
CURRENT APPLICATION NUMBER: US/10/410,962
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 45
LENGTH: 1203
TYPE: DNA
ORGANISM: Hepatitis B virus
US-10-410-962-45

Query Match 88.4%; Score 61; DB 17; Length 1203;
Best Local Similarity 92.8%; Pred. No. 2.5e-13;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACACTCTCTCTCAAGAACCTTATGTTTCCCTCATGTTGCTGTACAAACCTACGGAC 60
Db 895 ACGATTCCTCTCAAGAACCTTATGTTTCCCTCATGTTGCTGTACAAACCTACGGAC 954

QY 61 AGAAACTGC 69
Db 955 GGAAACTGC 963

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 16:17:45 ; Search time 1342 Seconds
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Listing first 45 summaries

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SUMMARIES

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TITLE
JOURNAL
COMMENT

The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine

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C	15	26.6	38.6	294	13	BQ091371	BQ091371 Kt16e05.Y
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C	19	26.6	38.6	444	12	BI502157	BI502157 Kt86a10.Y
C	20	26.6	38.6	447	12	BI450725	BI450725 Kt73h10.Y
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C	25	26.6	38.6	470	12	BI323090	BI323090 Kt61c07.Y
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ALIGNMENTS

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LOCUS
DEFINITION
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TO A PART OF THE TRIPLE-HELICAL REGION OF COLLAGEN ALPHA CHAIN. [1]
;contains element MSRI repetitive element ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

BG893479
BG893479.1 GI:14288089
EST.
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Strongyloides ratti
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidae; Strongyloidea; Strongyloides.
1 (bases 1 to 381)

REFERENCE
AUTHORS

McCartney, J., Clifton, S., Chiapelli, B., Pepe, D., Martin, J.,
Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagaris, V., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 The library was constructed by Brandi Chiapelli and Dr. James
 McCarter (bchiapell@watson.wustl.edu & jmcarter@watson.wustl.edu) at
 Washington University, St. Louis. DNA Sequencing by: Washington
 University Genome Sequencing Center St. Louis.
 High quality sequence stop: 379.

FEATURES

Location/Qualifiers
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 McCarter."
 /note="Vector: pAMP1 (Gibco); The library was constructed
 by Brandi Chiapelli and Dr. James McCarter at Washington
 University, St. Louis. The cDNA was made by using
 Dynabead oligo-dT priming (Dyna), PCR based library
 using a modified protocol from the SMART PCR cDNA
 Synthesis Kit from clontech. Directionally cloned into the
 UDG sites of pAMP1. Nematodes were provided by Dr. Mark
 Viney of Bristol, UK."

ORIGIN

Query Match 40.9%; Score 28.2; DB 12; Length 381;
 Best Local Similarity 68.4%; Pred. No. 25;
 Matches 39; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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RESULT 2

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 ACCESSION CS605031
 VERSION CS605031.1 GI:36921870
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 689)
 Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
 Rusch, D.B., Deicher, A.L., Pop, M., Wang, W., Fraser, C.M. and
 Venter, J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)
 22875432
 14512627
 CONTACT: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
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 Location/Qualifiers
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 /strain="Standard Poodle"
 /db_xref="taxon:9615"
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FEATURES

Location/Qualifiers
 1..689
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site_1: BstXI; Libraries were prepared from

ORIGIN

Query Match 40.6%; Score 28; DB 29; Length 689;
 Best Local Similarity 66.7%; Pred. No. 36;
 Matches 40; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 6 TCCTGCTCAAGAACCTCTATGTTTCCTCATGTTGCTGTACAAAACCTACGACAGAAA 65
 |||||
 DB 422 TCCTGCTCATGCTCACTCTCTCTTCTCCATGCTCTCAAAAAAAGAAAGAAA 481
 |||||

RESULT 3

CC184649 1068 bp DNA linear GSS 08-MAY-2003
 LOCUS CH261-10A21_RM1.1 CH261 Gallus gallus genomic clone CH261-10A21,
 DEFINITION genomic survey sequence.
 CC184649
 ACCESSION CC184649.1 GI:30428549
 VERSION CC184649
 KEYWORDS GSS.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 1068)
 Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
 Warren, W., Graves, T., Mardis, E. and Wilson, R.
 Gallus gallus BAC End Reads
 Unpublished (2003)
 Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@watson.wustl.edu
 Insert Length: 182000 Std Error: 0.00
 Seq primer: RM1 TACGACTCACTATAGGAGGA
 Class: BAC ends
 High quality sequence start: 37
 High quality sequence stop: 820.
 Location/Qualifiers
 1..1068
 /organism="Gallus gallus"
 /mol_type="genomic DNA"
 /strain="Red Jungle Fowl"
 /db_xref="taxon:9031"
 /clone="CH261-10A21"
 /sex="female"
 /cell_line="UCD001, inbred 256"
 /clone_lib="CH261"
 /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
 CH261 Female Chicken library - for library and clone
 ordering information: http://www.chori.org/bacpac"

FEATURES

Location/Qualifiers
 1..1068
 /organism="Gallus gallus"
 /mol_type="genomic DNA"
 /strain="Red Jungle Fowl"
 /db_xref="taxon:9031"
 /clone="CH261-10A21"
 /sex="female"
 /cell_line="UCD001, inbred 256"
 /clone_lib="CH261"
 /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
 CH261 Female Chicken library - for library and clone
 ordering information: http://www.chori.org/bacpac"

ORIGIN

Query Match 40.3%; Score 27.8; DB 28; Length 1068;
 Best Local Similarity 74.5%; Pred. No. 49;
 Matches 35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 7 CCTGCTCAAGAACCTCTATGTTTCCTCATGTTGCTGTACAAAACC 53
 |||||
 DB 966 CATGCCCCAGAAACCTGGTGTTTCCTTAGTTGCCCTCAAAACC 920
 |||||

RESULT 4

CC221988 1153 bp DNA linear GSS 12-MAY-2003
 LOCUS CH261-53N10_Sp6.1 CH261 Gallus gallus genomic clone CH261-53N10,
 DEFINITION genomic survey sequence.
 CC221988
 ACCESSION CC221988.1 GI:30546761
 VERSION CC221988
 KEYWORDS GSS.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1153)
REFERENCE
AUTHORS
  Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
  Warren, W., Graves, T., Mardis, E. and Wilson, R.
  Gallus gallus BAC End Reads
  Unpublished (2003)
  Genome Sequencing Center
  Washington University School of Medicine
  Email: submissions@watson.wustl.edu
  Insert Length: 182000 Std Error: 0.00
  Class: BAC ends
  Seq primer: Sp6 ATTAGTGACACTATAG
  High quality sequence start: 43
  High quality sequence stop: 705.
  Location/Qualifiers
    1..1153
      /organism="Gallus gallus"
      /mol_type="genomic DNA"
      /strain="Red Jungle Fowl"
      /db_xref="taxon:9031"
      /clone="CH261-53N10"
      /sex="female"
      /cell_line="UCD001, inbred 256"
      /clone_lib="CH261"
      /notes="Vector: pPARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
      CH261 Female Chicken library - for library and clone
      ordering information: http://www.chori.org/bacpac"
ORIGIN
source
Query Match 40.0%; Score 27.6; DB 28; Length 1153;
Best Local Similarity 63.6%; Pred. No. 59; Indels 0; Gaps 0;
Matches 42; Conservative 0; Mismatches 24;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 60
Db 750 AAAACTCTGCTCAGGACCTCCGCTTCCCTCAGGTGGAACCTATAAACTGCTATG 803
QY 61 AGAAAC 66
Db 810 AGAACC 815

RESULT 5
CC286213/c
LOCUS
DEFINITION
  CC286213 1254 bp DNA linear GSS 13-MAY-2003
  genomic survey sequence.
ACCESSION
  CC286213
VERSION
  CC286213.1 GI:30655514
KEYWORDS
  GSS.
SOURCE
  Gallus gallus (chicken)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
    Phasianinae; Gallus.
REFERENCE
  1 (bases 1 to 1254)
  Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
  Warren, W., Graves, T., Mardis, E. and Wilson, R.
  Gallus gallus BAC End Reads
  Unpublished (2003)
  Contact: Richard K. Wilson
  Genome Sequencing Center
  Washington University School of Medicine
  Email: submissions@watson.wustl.edu
  Insert Length: 182000 Std Error: 0.00
  Class: BAC ends
  Seq primer: Sp6 ATTAGTGACACTATAG
  High quality sequence start: 288
  High quality sequence stop: 814.
  Location/Qualifiers
    1..1254
      /organism="Gallus gallus"
      /mol_type="genomic DNA"
      /strain="Red Jungle Fowl"
      /db_xref="taxon:9031"
      /clone="CH261-2911"
      /sex="female"
      /cell_line="UCD001, inbred 256"
      /clone_lib="CH261"
      /notes="Vector: pPARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
      CH261 Female Chicken library - for library and clone
      ordering information: http://www.chori.org/bacpac"
ORIGIN
source
Query Match 40.0%; Score 27.6; DB 28; Length 1254;
Best Local Similarity 67.2%; Pred. No. 50; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 19;

QY 8 CTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGACGAAA 65
Db 311 CAGCAAAAGAGGGTATATGTTCTCTCACATTACTGTATGAATGTAATTACATAA 254

RESULT 6
BZ089079/c
LOCUS
DEFINITION
  BZ089079 792 bp DNA linear GSS 10-OCT-2002
  1k155g04.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
  sequence.
ACCESSION
  BZ089079
VERSION
  BZ089079.1 GI:23723714
KEYWORDS
  GSS.
SOURCE
  Brassica oleracea
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 792)
  Delehaanty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,
  Nash, W., Rabinowicz, P.D. and Wilson, R.K.
  Whole genome shotgun reads from Brassica oleracea
  Unpublished (2002)
  Contact: Richard K. Wilson
  Genome Sequencing Center
  Washington University School of Medicine
  Email: submissions@watson.wustl.edu
  Plate: 1k155 row: g column: 04
  Seq primer: -28RpPOT reverse
  Class: shotgun
  High quality sequence start: 12
  High quality sequence stop: 447.
  Location/Qualifiers
    1..792
      /organism="Brassica oleracea"
      /mol_type="genomic DNA"
      /db_xref="taxon:3712"
      /clone_lib="B.oleracea002"
      /notes="Vector: POTw13; Whole genome shotgun library from
      flowering buds. DNA was purified from a crude nuclear
      prep using Brassica oleracea T0100DH3 buds, provided by
      Thomas Osborn at the University of Wisconsin. Genomic
      DNA was provided by Pablo Rabinowicz (CSHL) and the
      shotgun library prepared at Washington University Genome
      Sequencing Center."
ORIGIN
source
Query Match 39.7%; Score 27.4; DB 28; Length 792;
Best Local Similarity 69.8%; Pred. No. 62; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 16;

QY 14 AGGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGACGACAAAAC 66
Db 703 ATGGAGCCATTGTGTTCCCGAATGTTGGGTCCTTTCGAAGAAAC 651

```

RESULT 7
 BY615763/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BY615763 415 bp mRNA linear EST 15-DEC-2002
 BY615763 RIKEN full-length enriched, visual cortex Mus musculus
 CDNA clone K330012B19 3', mRNA sequence.
 BY615763
 BY615763.1 GI:26950945
 EST.
 Mus musculus (house mouse)

Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 415)

REFERENCE
 AUTHORS
 CONTACT: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Inotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT

3 AACTCCTGCTCAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAACCTACGACAG 62
 122 AACACGGGCACAGGCAAGTTTACATTTTACACACAGTTTCCCTCCACCTACCCACAG 63
 63 AACAC 66
 62 AACAC 59

Query Match 39.4%; Score 27.2; DB 13; Length 415;
 Best Local Similarity 64.1%; Pred. No. 60;
 Matches 41; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

ORIGIN
 Location/Qualifiers
 1..415
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="K330012B19"
 /tissue_type="visual cortex"
 /clone_lib="RIKEN full-length enriched, visual cortex"

FEATURES
 source
 1..415
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="K330012B19"
 /tissue_type="visual cortex"
 /clone_lib="RIKEN full-length enriched, visual cortex"

CC875918 693 bp DNA linear GSS 29-JUL-2003
 ZMWBB019N08.f ZMWBBB Zea mays subsp. mays genomic clone
 ZMWBB019N08 5', genomic survey sequence.
 CC875918
 CC875918.1 GI:33305593
 GSS.
 Zea mays subsp. mays (maize)
 Zea mays subsp. mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoideae; Andropogoneae; Zea.
 Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.
 and Wing, R.
 Sequencing of the maize genome
 Unpublished (2003)
 Contact: Rod Wing
 Arizona Genomics Institute
 University of Arizona
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
 85721-0088, USA
 Tel: 520 626 3967
 Fax: 520 621 9288
 Email: http://genome.arizona.edu
 PCR Primers
 FORWARD: T7
 BACKWARD: M13r
 Plate: 0190 row: N column: 08
 Seg primer: T7
 Class: BAC ends.
 Location/Qualifiers
 1..693
 /organism="Zea mays subsp. mays"
 /mol_type="genomic DNA"
 /cultivar="B73"
 /sub_species="mays"
 /db_xref="taxon:4578"

```

/clone="ZMMBB0190N08"
/lab_host="DH103"
/clone_lib="ZMMBB"
/notes=vector: pBeloBAC11; Site 1: HindIII; Site 2:
HindIII; Zea mays L. ssp. mays"
ORIGIN
Query Match      39.1%; Score 27; DB 29; Length 693;
Best Local Similarity 70.6%; Pred. No. 82;
Matches 36; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2 CAATCTCTGCTCAGGAACTCTATGTTTCCCTCATGTTCTGTACAAAC 52
Db 680 CAATCTCTGTTGAATACTATCTGTGCTTCACTCACTTCGGCTCTTAC 630

RESULT 9
BZ965578 840 bp DNA linear GSS 25-MAR-2003
LOCUS PUGGM72TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa379K23,
DEFINITION Genomic survey sequence.
ACCESSION BZ965578
VERSION BZ965578.1 GI:29181484
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 840)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Other GSSs: PUGGM72TB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: Tg
Class: sheared ends.
FEATURES
source
1..840
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa379K23"
/clone_lib="ZM_0.6_1.0_KB"
/notes=vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"
ORIGIN
Query Match      39.1%; Score 27; DB 28; Length 840;
Best Local Similarity 62.7%; Pred. No. 87;
Matches 42; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAGGAACTCTATGTTTCCCTCATGTTCTGTACAAACCTACGGAC 60
Db 233 ACAACTAGCTGTACGGCAACTCTATGTTTCCCTGTAGTGTATGGCCACCATGGTC 174

QY 61 AGAAACT 67
Db 173 GTTACCT 167

RESULT 10
AQ752847 745 bp DNA linear GSS 19-JUL-1999
LOCUS HS_5570_B1_B01_SP6 RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION

```

```

genomic clone Plate=1146 Col=1 Row=D, genomic survey sequence.
ACCESSION AQ752847 GI:5540005
VERSION AQ752847.1
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 745)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1146 row: D column: 1
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 745.
FEATURES
source
1..745
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=1146 Col=1 Row=D"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/notes=vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
ORIGIN
Query Match      38.8%; Score 26.8; DB 28; Length 745;
Best Local Similarity 64.5%; Pred. No. 99;
Matches 40; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 4 ACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGTGTACAAACCTACGGACAGA 63
Db 7 ACTGCTGGGAACAATTCATCTGCACTTTCATGTTCTGCACAGAACTTCTGACCAA 66

QY 64 AA 65
Db 67 AA 68

RESULT 11
CG901218 785 bp DNA linear GSS 09-DEC-2003
LOCUS ZMMBB0508G03f ZMMBBb (HindIII) Zea mays subsp. mays genomic clone
DEFINITION ZMMBBb0508G03 5', genomic survey sequence.
ACCESSION CG901218
VERSION CG901218.1 GI:39600485
KEYWORDS GSS.
SOURCE Zea mays subsp. mays (maize)
ORGANISM Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 785)
Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C., Zohovetz, V., Fuks, G., Yu, Y., Wing, R. and Messing, J.

Sequencing of the maize genome at PGIR (2003c)
Unpublished (2003)

CONTACT: Bharti, A.K.

Dr. Joachim Messing's lab

The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers

University

190 Frelinghuysen Road, Piscataway, NJ 08854, USA

Tel: 732 445 3801

Fax: 732 445 5735

Email: bharti@waksman.rutgers.edu

Seq primer: T7

Class: BAC ends

High quality sequence start: 116.

Location/Qualifiers

1..785

/organism="Zea mays subsp. mays"

/mol_type="genomic DNA"

/cultivar="B73"

/sub_species="mays"

/db_xref="taxon:4578"

/clone="ZMMBB0508G03"

/lab_host="E. coli DH10B"

/clone_lib="ZMMBBB (HindIII)"

/note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 38.8%; Score 26.8; DB 29; Length 785;

Best Local Similarity 64.5%; Pred. No. 1e+02;

Matches 40; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 3 AACCTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGACAG 62

Db 311 AACCTTTCACAAAGACTCTGATGTTTCACCTTAATCCCTTTCAAAACCTTCGACTC 370

QY 63 AA 64

Db 371 AA 372

CG398694 1021 bp DNA linear GSS 22-SEP-2003

ZMMBB0019E20f ZMMBBc (EcoRI) Zea mays subsp. mays genomic clone

CG398694 5', genomic survey sequence.

CG398694.1 GI:34342709

GSS.

Zea mays subsp. mays (maize)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 1021)

Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,

Rouzaud, K., Fuks, G., Yu, Y., Wing, R. and Messing, J.

Sequencing of the maize genome at PGIR (2003b)

Unpublished (2003)

CONTACT: Bharti, A.K.

Dr. Joachim Messing's lab

The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers

University

190 Frelinghuysen Road, Piscataway, NJ 08854, USA

Tel: 732 445 3801

Fax: 732 445 5735

Email: bharti@waksman.rutgers.edu

Seq primer: T7

Class: BAC ends

High quality sequence start: 57.

FEATURES
source

1..1021

/organism="Zea mays subsp. mays"

/mol_type="genomic DNA"

/cultivar="B73"

/sub_species="mays"

/db_xref="taxon:4578"

/clone="ZMMBBc0019E20"

/lab_host="E. coli DH10B"

/clone_lib="ZMMBBc (EcoRI)"

/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN

Query Match 38.8%; Score 26.8; DB 29; Length 1021;

Best Local Similarity 64.5%; Pred. No. 1.1e+02;

Matches 40; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 3 AACCTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGACAG 62

Db 306 AACCTTTCACAAAGACTCTATGTTTCACCTTAATCCCTTTCAAAACCTTCGACCC 365

QY 63 AA 64

Db 366 AA 367

BI073599 259 bp mRNA linear EST 19-JUN-2001

KT32f12.Y1 Strongyloides ratti L2 pAMP1 v1 Chiapelli McCarter

Strongyloides ratti cDNA 5', similar to TR:Q19528 Q19528 F1C8.2

PROTEIN: [1]; contains element PTR7 repetitive element ;, mRNA

sequence.

BI073599.1 GI:14494219

EST.

Strongyloides ratti

Strongyloides ratti

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

Panagrolaimoidea; Strongyloidea; Strongyloides.

1 (bases 1 to 259)

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,

Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,

Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,

Teagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,

Harwood, K., Steptoe, M., Allen, M., Kohn, S., Shin, T., Jackson, Y.,

McCann, R., Waterston, R. and Wilson, R.

The Washington Univ. Nematode EST Project, 1999

Unpublished (1999)

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

The library was constructed by Brandi Chiapelli and Dr. James

McCarter (bchiapelle@wustl.edu & jmcarter@wustl.edu) at

Washington University, St. Louis. DNA Sequencing by: Washington

University Genome Sequencing Center St. Louis.

Seq primer: -40RP from Gibco

High quality sequence stop: 191.

Location/Qualifiers

1..259

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/mol_type="mRNA"

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/dev_stage="L2"

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/clone_lib="Strongyloides ratti L2 pAMP1 v1 Chiapelli

McCarter"

/note="Vector: pAMP1 (Gibco); The library was constructed

FEATURES
source

1..259

/organism="Strongyloides ratti"

/mol_type="mRNA"

/db_xref="taxon:34506"

/dev_stage="L2"

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McCarter"

/note="Vector: pAMP1 (Gibco); The library was constructed

by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dyna). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Nematodes were provided by Dr. Mark Viney of Bristol, UK.

ORIGIN

Query Match 38.6%; Score 26.6; DB 12; Length 259;
Best Local Similarity 66.7%; Pred. No. 84;
Matches 38; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 12 TCAAGGAACTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGACAGAACTG 68
Db 81 TCAATGAACCTCGTATTCGTTCTCATGTTGCTGTACAAAATTTCCGTCGTAAC 137

RESULT 14
LOCUS BQ091116 294 bp mRNA linear EST 05-APR-2002
DEFINITION ku13b03.y1 Strongyloides ratti L2 pAMP1 v1 Chiapelli McCarter
Strongyloides ratti cDNA 5' similar to TR:Q17418 Q17418 B0024.2
PROTEIN. [1]; contains element MSR1 repetitive element ;, mRNA
sequence.
ACCESSION BQ091116
VERSION BQ091116.1 GI:20065317
KEYWORDS EST
SOURCE Strongyloides ratti
ORGANISM Strongyloides ratti
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimidae; Strongyloidea; Strongyloides.
REFERENCE 1 (bases 1 to 294)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
Wyllie,T., Dante,M., Marz,M., Hillier,L., Kucaba,T., Theising,B.,
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
Tsagarisshvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
CONTACT: McCarter JP

TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished (1999)
COMMENT The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at
Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
Location/Qualifiers

FEATURES
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McCarter"
/note="Vector: pAMP1 (Gibco); The library was constructed
by Brandi Chiapelli and Dr. James McCarter at Washington
University, St. Louis. The cDNA was made by using
Dynabead oligo-dT priming (Dyna). PCR based library
using a modified protocol from the SMART PCR cDNA
Synthesis Kit from Clontech. Directionally cloned into the
UDG sites of pAMP1. Nematodes were provided by Dr. Mark
Viney of Bristol, UK."

ORIGIN

Query Match 38.6%; Score 26.6; DB 13; Length 294;

Best Local Similarity 66.7%; Pred. No. 88;
Matches 38; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 12 TCAAGGAACTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGACAGAACTG 68
Db 110 TCAATGAACCTCGTATTCGTTCTCATGTTGCTGTACAAAATTTCCGTCGTAAC 166

ORIGIN

RESULT 15
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DEFINITION ku16e05.y1 Strongyloides ratti L2 pAMP1 v1 Chiapelli McCarter
Strongyloides ratti cDNA 5' similar to TR:Q17418 Q17418 B0024.2
PROTEIN. [1]; contains element MSR1 repetitive element ;, mRNA
sequence.
ACCESSION BQ0911371
VERSION BQ0911371.1 GI:20065572
KEYWORDS EST
SOURCE Strongyloides ratti
ORGANISM Strongyloides ratti
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimidae; Strongyloidea; Strongyloides.
REFERENCE 1 (bases 1 to 294)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
Wyllie,T., Dante,M., Marz,M., Hillier,L., Kucaba,T., Theising,B.,
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
Tsagarisshvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
CONTACT: McCarter JP

TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished (1999)
COMMENT The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at
Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
Location/Qualifiers

FEATURES
source 1..294
/organism="Strongyloides ratti"
/mol_type="mRNA"
/db_xref="taxon:34506"
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/lab_host="DH10B"
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McCarter"
/note="Vector: pAMP1 (Gibco); The library was constructed
by Brandi Chiapelli and Dr. James McCarter at Washington
University, St. Louis. The cDNA was made by using
Dynabead oligo-dT priming (Dyna). PCR based library
using a modified protocol from the SMART PCR cDNA
Synthesis Kit from Clontech. Directionally cloned into the
UDG sites of pAMP1. Nematodes were provided by Dr. Mark
Viney of Bristol, UK."

ORIGIN

Query Match 38.6%; Score 26.6; DB 13; Length 294;
Best Local Similarity 66.7%; Pred. No. 88;
Matches 38; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 12 TCAAGGAACTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGACAGAACTG 68
Db 110 TCAATGAACCTCGTATTCGTTCTCATGTTGCTGTACAAAATTTCCGTCGTAAC 166

Search completed: July 26, 2004, 17:28:08
Job time : 1346 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 12:21:09 ; Search time 3003 Seconds
(without alignments)
9829.040 Million cell updates/sec

Title: US-09-719-533A-1_COPY_155_835

Perfect score: 681
Sequence: 1 ATGAGAACATCCATCAGG.....GTCTTTGGGTATACATTAA 681

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 347072 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	681	100.0	3215	6	BD232230	BD232230 Hepatitis
2	676.2	99.3	3215	14	AB073834	AB073834 Hepatitis
3	676.2	99.3	3215	14	AF100308	AF100308 Hepatitis
4	676.2	99.3	3215	14	AF100309	AF100309 Hepatitis
5	676.2	99.3	3215	14	AF121243	AF121243 Hepatitis
6	676.2	99.3	3215	14	AF121245	AF121245 Hepatitis
7	676.2	99.3	3215	14	AF121246	AF121246 Hepatitis
8	676.2	99.3	3215	14	AF167097	AF167097 Hepatitis
9	674.6	99.1	3215	14	AB073822	AB073822 Hepatitis
10	674.6	99.1	3215	14	AB073827	AB073827 Hepatitis
11	674.6	99.1	3215	14	AB073828	AB073828 Hepatitis
12	674.6	99.1	3215	14	AF121244	AF121244 Hepatitis
13	674.6	99.1	3215	14	AF121249	AF121249 Hepatitis
14	674.6	99.1	3215	14	AF282918	AF282918 Hepatitis
15	674.6	99.1	3215	14	AF479684	AF479684 Hepatitis
16	674.6	99.1	3215	14	HEVP6CSX	X97851 Hepatitis B
17	673.8	98.9	3215	14	AB073840	AB073840 Hepatitis
18	673	98.8	1431	14	AF291830	AF291830 Hepatitis
19	673	98.8	1758	14	AF279464	AF279464 Hepatitis
20	673	98.8	3215	14	AB073826	AB073826 Hepatitis
21	673	98.8	3215	14	AF167089	AF167089 Hepatitis
22	673	98.8	3215	14	AY220703	AY220703 Hepatitis
23	673	98.8	3215	14	HPBADW2	D00330 Hepatitis B
24	672.2	98.7	3215	14	AB073821	AB073821 Hepatitis
25	671.4	98.6	681	14	AF061527	AF061527 Hepatitis
26	671.4	98.6	681	14	AF397207	AF397207 Hepatitis
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28	671.4	98.6	3213	14	AY217369	AY217369 Hepatitis
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30	671.4	98.6	3215	14	AY217356	AY217356 Hepatitis
31	671.4	98.6	3215	14	AY217362	AY217362 Hepatitis
32	671.4	98.6	3248	14	AY206377	AY206377 Hepatitis
33	671	98.5	3215	14	AB073831	AB073831 Hepatitis
34	671	98.5	3215	14	AF167094	AF167094 Hepatitis
35	670.2	98.4	3215	14	AF121247	AF121247 Hepatitis
36	669.8	98.4	681	6	AR026126	AR026126 Sequence
37	669.8	98.4	681	6	AR026128	AR026128 Sequence
38	669.8	98.4	3212	14	AY217365	AY217365 Hepatitis
39	669.8	98.4	3214	14	HBV131133	AJ131133 Hepatitis
40	669.8	98.4	3215	14	AB073841	AB073841 Hepatitis
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ALIGNMENTS

RESULT 1

BD232230

LOCUS

DEFINITION

Hepatitis B virus strains appearing by vaccine administration and

utilization thereof.

ACCESSION

BD232230

VERSION

BD232230.1 GI:33042000

KEYWORDS

JP 2002518013-A/1.

SOURCE

unidentified

ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 3215)

AUTHORS

Oon,C.J., Lim,G.K., Leong,A.L., Zhao,Y. and Chen,W.N.

TITLE

Hepatitis B virus strains appearing by vaccine administration and

utilization thereof

BD232230 3215 bp DNA linear PAT 17-JUL-2003
Hepatitis B virus strains appearing by vaccine administration and
utilization thereof.

JOURNAL	Patent: JP 2002518013-A 1 25-JUN-2002;	Db	755	TGGGGCCAGTCTGTACACATCTTGAGTCCTTTATGCGCTGTACCAATTTCTTT 814
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PN	JP 2002518013-A/1			
PD	25-JUN-2002			
PF	19-JUN-1998 JP 2000554856			
PI	CHONG JIN GEK KEOW LIM, AI LIN LEONG, YI ZHAO, WEI NING CHEN			
PC	C12N15/09, A61K39/29, A61K45/00, A61P1/16, A61P31/20, A61P35/00, PC C07K14/02,			
PC	C07K16/08, C12N7/00, C12P21/02, C12P21/08, C12Q1/68, G01N33/53, PC G01N33/53,			
PC	G01N33/566, G01N33/576, C12N15/00			
CC	Strandedness: Double;			
CC	Topology: Circular;			
CC	Hepatitis B virus strains appearing by vaccine administration			
CC	and			
CC	utilization thereof			
CC	Location/Qualifiers			
FF	Key			
FT	source			
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Qy	121 TTCTAGGGGGAACACCGGTGTCTTGGCCAAAATCCGAGTCCCAAAATCTCCAGTCCAC 180			
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Db	575 AAACCTAGGACGAACTGCACTGATTTCCCATCCCATCATCTTCCGCTTTTCGCAAAA 634			
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Qy	661	TGCTTTGGGTATACATTTAA 681
Db	815	TGCTTTGGGTATACATTTAA 835
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LOCUS		
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ACCESSION	AB073834	
VERSION	AB073834.1	
KEYWORDS	GI:21280253	
SOURCE	Hepatitis B virus	
ORGANISM	Hepatitis B virus	
REFERENCE	1	
AUTHORS	Sugauchi, F., Orito, E., Ichida, T., Kato, H., Sakugawa, H., Kakumu, S., Ishida, T., Chutaputti, A., Lai, C.L., Ueda, R., Miyakawa, Y. and Mizokami, M.	
TITLE	Hepatitis B virus of genotype B with or without recombination with genotype C over the precore region plus the core gene	
JOURNAL	J. Virol. 76 (12), 5985-5992 (2002)	
MEDLINE	22016130	
PUBMED	12021331	
REFERENCE	2 (bases 1 to 3215)	
AUTHORS	Sugauchi, F., Orito, E., Kato, H., Ueda, R. and Mizokami, M.	
TITLE	Direct Submission	
JOURNAL	Submitted (01-NOV-2001) Fuminaka Sugauchi, Nagoya City University Medical School Graduate School of Science, Department of Internal Medicine and Molecular Science, Mizuho, Nagoya, Aichi 467-8601, Japan (E-mail: suga@med.nagoya-cu.ac.jp, Tel:81-52-853-8216, Fax:81-52-842-0021)	
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ORIGIN		
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Db	155 ATGGAGAACATCGCATCAGGACTCTAGGACCCCTGCTGCTGTGTTACAGCGGGTTTTC 214	
Qy	61 TTGTTGACAAAATCCTCACAAATCCGAGAGTCTAGACTCGTGGTGGACTTCTCAAT 120	
Db	215 TTGTTGACAAAATCCTCACAAATCCGAGAGTCTAGACTCGTGGTGGACTTCTCAAT 274	
Qy	121 TTCTAGGGGGAACACCGGTGTCTTGGCCAAAATCCGAGTCCCAAAATCTCCAGTCCAC 180	
Db	275 TTCTAGGGGGAACACCGGTGTCTTGGCCAAAATCCGAGTCCCAAAATCTCCAGTCCAC 334	
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Qy      361 TGCAAAACCTGCAACAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 420
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Qy      421 AAACCTACGACGAGAACTGACCTGATATCCCATCCCATCATCTTGGGCTTTCGCAAAA 480
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Qy      661 TGCTTTTGGGTATACATTTAA 681
Db      817 TGCTTTTGGGTATACATTTAA 837

RESULT 5
AF121243
LOCUS      3215 bp      DNA      circular VRL 27-FEB-2001
DEFINITION Hepatitis B virus isolate HBV/14611, complete genome.
ACCESSION AF121243
VERSION    AF121243.1 GI:6692482
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS      Hannoun,C., Hoxal,P. and Lindh,M.
TITLE      Long-term mutation rates in the hepatitis B virus genome
JOURNAL      J. Gen. Virol. 81 (Pt 1), 75-83 (2000)
MEDLINE      20109034
PUBMED      10640544
REFERENCE    2 (bases 1 to 3215)
AUTHORS      Hannoun,C., Hoxal,P. and Lindh,M.
TITLE      Direct Submission
JOURNAL      Submitted (19-JAN-1999) Clinical Virology, Laboratory Medicine,
Guldhedsgatan 10B, Goteborg 413 46, Sweden
FEATURES
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ORIGIN

Query Match 99.3%; Score 676.2; DB 14; Length 3215;
Best Local Similarity 99.6%; Pred. No. 2.4e-187;
Matches 678; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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KEYWORDS Hepatitis B virus
SOURCE Hepatitis B virus
ORGANISM Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE 1 (bases 1 to 3215)
AUTHORS Hannoun, C., Horal, P. and Lindh, M.
TITLE Long-term mutation rates in the hepatitis B virus genome.
JOURNAL J. Gen. Virol. 81 (Pt 1), 75-83 (2000)
MEDLINE 20109034
PUBMED 10640544
REFERENCE 2 (bases 1 to 3215)
AUTHORS Hannoun, C., Horal, P. and Lindh, M.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-1999) Clinical Virology, Laboratory Medicine,
Guldhedsgatan 10B, Goteborg 413 46, Sweden
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ACCESSION AF121245
VERSION AF121245.1 GI:6692484

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           Guldhedsatan 10B, Goteborg 413 46, Sweden
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ORIGIN

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Query Match      99.3%; Score 676.2; DB 14; Length 3215;
Best Local Similarity 99.6%; Pred. No. 2.4e-187;
Matches 678; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DEFINITION Hepatitis B virus isolate Iiib, complete genome.
ACCESSION AY167097
VERSION AY167097.1 GI:32346284
KEYWORDS
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SOURCE
Hepatitis B virus
ORGANISM
Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
REFERENCE
1 (bases 1 to 3215)
AUTHORS
Liu, C.-J., Chen, P.-J., Lai, M.-Y., Kao, J.-H. and Chen, D.-S.
TITLE
A prospective study characterizing full-length hepatitis B virus genomes during acute exacerbation
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 3215)
AUTHORS
Liu, C.-J., Chen, P.-J., Lai, M.-Y., Kao, J.-H. and Chen, D.-S.
TITLE
Direct Submission
JOURNAL
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Query Match 99.3%; Score 576.2; DB 14; Length 3215;
Best Local Similarity 99.6%; Pred. No. 2.4e-187;
Matches 678; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAGAACATCGCATCAGGACTCTAGGACCCCTGCTGTTTACAGGGGGGTTTTTC 60
DB 155 ATGAGAACATCGCATCAGGACTCTAGGACCCCTGCTGTTTACAGGGGGGTTTTTC 214

QY 61 TTGTGTGACAAAATTCCTCAACATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCAAT 120
DB 215 TTGTGTGACAAAATTCCTCAACATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCAAT 274
QY 121 TTCTAGGGGGAACACCCGCTGTGTCTTGGCCAAAATTCGCAGATCCCAAATCTCCAGTCAC 180
DB 275 TTCTAGGGGGAACACCCGCTGTGTCTTGGCCAAAATTCGCAGATCCCAAATCTCCAGTCAC 334
QY 181 TCACCAACCTGTGTCTCTCAAAATTTGCTTGGTATCGCTGGATGTCTCGCGCGTTTTT 240
DB 335 TCACCAACCTGTGTCTCTCAAAATTTGCTTGGTATCGCTGGATGTCTCGCGCGTTTTT 394
QY 241 ATCATCTCTCTGCATCCCTGCTATGCTCATCTCTTCTTGGTGTCTTCTTGGACTAT 300
DB 395 ATCATCTCTCTGCATCCCTGCTATGCTCATCTCTTCTTGGTGTCTTCTTGGACTAT 454
QY 301 CAAGGTATGTTGCCCGTTTGTCTCTTAATTCAGGATCAACAAACACGACCCGACCA 360
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QY 421 AAACCTACGGACAGAAAATGCACCTGTATTCCCATCCCATCATCTTGGGCTTTCGAAAA 480
DB 575 AAACCTACGGACAGAAAATGCACCTGTATTCCCATCCCATCATCTTGGGCTTTCGAAAA 634
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QY 541 CAGTGGTTCGTAGGGCTTTCGCCCACTGTCTGGCTTTCAGTTATATGATGATGTTGTT 600
DB 695 CAGTGGTTCGTAGGGCTTTCGCCCACTGTCTGGCTTTCAGTTATATGATGATGTTGTT 754
QY 601 TGGGGCCCAAGTCTGTACAAACATCTAGTCCCTTTATGCGCTGTACCAATTTCTTT 660
DB 755 TGGGGCCCAAGTCTGTACAAACATCTAGTCCCTTTATGCGCTGTACCAATTTCTTT 814
QY 661 TGTCTTTCGGTATACATTTAA 681
DB 815 TGTCTTTCGGTATACATTTAA 835

RESULT 9
AB073822
LOCUS
DEFINITION
Hepatitis B virus DNA, complete genome, isolate:HBV-Chi32.
ACCESSION
AB073822
VERSION
AB073822.1
GI:21280229
KEYWORDS
Hepatitis B virus
Hepatitis B virus
ORGANISM
Viruses; Retroviridae; Orthohepadnavirus.
REFERENCE
1
Sugauchi, F., Orito, E., Ichida, T., Kato, H., Sakugawa, H., Kakumu, S.,
Ishida, T., Chutaputti, A., Lai, C.L., Ueda, R., Miyakawa, Y. and
Mizokami, M.
Hepatitis B virus of genotype B with or without recombination with
genotype C over the precore region plus the core gene
J. Virol. 76 (12), 5985-5992 (2002)
22016130
MEDLINE
12021331
PUBMED
REFERENCE
2 (bases 1 to 3215)
AUTHORS
Sugauchi, F., Orito, E., Kato, H., Ueda, R. and Mizokami, M.
TITLE
Direct Submission
JOURNAL
Submitted (01-Nov-2001) Fuminaka Sugauchi, Nagoya City University
Medical School Graduate School of Science, Department of Internal
Medicine and Molecular Science, Mizuho, Nagoya, Aichi 467-8601,
Japan [E-mail:sugamed.nagoya-cu.ac.jp, Tel:81-52-853-8216,
Fax:81-52-842-0021]

ORIGIN

Query Match 99.1%; Score 674.6; DB 14; Length 3215;
Best Local Similarity 99.4%; Pred. No. 7.2e-187;
Matches 677; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 61 TTGTGTCAAAATTCCTCAAAATTCCTCAAAATTCCTCAAAATTCCTCAAAATTCCTCAAA 120
DB 215 TTGTGTCAAAATTCCTCAAAATTCCTCAAAATTCCTCAAAATTCCTCAAAATTCCTCAAA 274
QY 121 TTCTAGGGGAAACACCGGTGTGCTTGGCCAAATTCGAGTCCCAAAATTCGAGTCCCA 180
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QY 421 AAACCTACGGACAGAACTGCACCTGTATCCCATCCCATCATCTTGGGCTTTTCGCAAAA 480
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QY 541 CAGTGGTTCGTAGGGCTTTTCCCGCACTCTCTGGCTTTTCCAGTTATATGATGATGTTGTT 600
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QY 601 TGGGGGCGCAAGTCTGTACAACTCTTGTAGTCCCTTTATGCGCTGTACCAATTTCTTT 660
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QY 661 TGTCTTTGGGTATACATTAA 681
DB 815 TGTCTTTGGGTATACATTAA 835

RESULT 12

AF121244
LOCUS Hepatitis B virus isolate HBV/15122, complete genome.
DEFINITION AF121244
ACCESSION AF121244
VERSION AF121244.1 GI:6692483
KEYWORDS
SOURCE Hepatitis B virus
ORGANISM Hepatitis B virus
VIRUSES; Retrovirus; Hepadnaviridae; Orthohepadnavirus.
REFERENCE 1 (bases 1 to 3215)
AUTHORS Hannoun, C., Horal, P. and Lindh, M.
TITLE Long-term mutation rates in the hepatitis B virus genome
JOURNAL J. Gen. Virol. 81 (Pt 1), 75-83 (2000)
MEDLINE 20109034
PUBMED 10640544

QY 301 CAAGGTATGTTGCGCGCTTGTCTCTAATTCAGGATCAACAAACACGACCGGACCA 360
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DB 515 TCGAAACCTGCAACAACTCTGCTCAAGAACCTCTATGTTTCCCTCATGTTGCTGTACA 574
QY 421 AAACCTACGGACAGAACTGCACCTGTATCCCATCCCATCATCTTGGGCTTTTCGCAAAA 480
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DB 815 TGTCTTTGGGTATACATTAA 835

RESULT 11

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DEFINITION AB073828
ACCESSION AB073828
VERSION AB073828.1 GI:21280241
KEYWORDS
SOURCE Hepatitis B virus
ORGANISM Hepatitis B virus
VIRUSES; Retrovirus; Hepadnaviridae; Orthohepadnavirus.
REFERENCE 1
AUTHORS Sugauchi, F., Orito, E., Ichida, T., Kato, H., Sakugawa, H., Kakumu, S., Ikenida, T., Churaputti, A., Lai, C.L., Ueda, R., Miyakawa, Y. and Mizokami, M.
TITLE Hepatitis B virus of genotype B with or without recombination with genotype C over the precore region plus the core gene
JOURNAL J. Virol. 76 (12), 5985-5992 (2002)
MEDLINE 22016130
PUBMED 12021331
REFERENCE 2 (bases 1 to 3215)
AUTHORS Sugauchi, F., Orito, E., Kato, H., Ueda, R. and Mizokami, M.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2001) Fuminaka Sugauchi, Nagoya City University Medical School Graduate School of Science, Department of Internal Medicine and Molecular Science; Mizuho, Nagoya, Aichi 467-8601, Japan (E-mail: suga@med.nagoya-cu.ac.jp, Tel:81-52-853-8216, Fax:81-52-842-0021)
FEATURES
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REFERENCE 2 (bases 1 to 3215)
AUTHORS Hannoun, C., Horal, P. and Lindh, M.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-1999) Clinical Virology, Laboratory Medicine,
Guilhedsgatan 10B, Goteborg 413 46, Sweden
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PSRRRSQSPRRRSQSRQSC"
ORIGIN
Query Match 99.1%; Score 674.6; DB 14; Length 3215;
Best Local Similarity 99.4%; Pred. No. 7.2e-187;
Matches 677; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 ATGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTGTGTGTACAGGCGGGTTTTTC 60
DB 155 ATGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTGTGTGTACAGGCGGGTTTTTC 214
QY 61 TTGTTGACAAAATCCTCACAATAACGACAGTCTAGACTCGTGTGACTTCTCTCAAT 120
DB 215 TTGTTGACAAAATCCTCACAATAACGACAGTCTAGACTCGTGTGACTTCTCTCAAT 274
QY 121 TTTCTAGGGGGAACACCCGTGTGTCTTGGCCAAAATTCGAGTCCCAAAATCTCCAGTCAC 180
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QY 181 TCACCAACCTGTGTCTCCCAATTTGCTGTGTATCGCTGGATGTCTGCGCGGTTTT 240
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QY 241 ATCATCTTCTCTGCACTCTGCTGTATGCTCATCTTCTTGTGTGTCTTCTCGGACTAT 300
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QY 361 TCGAAAACCTGCACAACTCTCTCAAGGAACCTCTATGTTTCCCTCATGTTCTCTGATCA 420
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Db 575 AAACCTACGACGGAACATGACCTGTATCCATCCCATCATCTTGGCTTCCAAA 634
Qy 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTGCTCAGTTACTAGTCCATTGTT 540
Db 635 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTGCTCAGTTACTAGTCCATTGTT 694
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Db 755 TGGGGGCCAAGTCTGTACAACTCTGAGTCCCTTTATGCCCTGTTACCAATTTCTTT 814
Qy 661 TGTCTTTGGGTATACATTTAA 681
Db 815 TGTCTTTGGGTATACATTTAA 835

RESULT 13
LOCUS AF121249 3215 bp DNA circular VPL 27-FEB-2001
DEFINITION Hepatitis B virus isolate HBV/4014, complete genome.
ACCESSION AF121249
VERSION AF121249.1 GI:6692488
KEYWORDS
SOURCE Hepatitis B virus
ORGANISM Hepatitis B virus
VIRUSES; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE 1 (bases 1 to 3215)
Hannoun,C., Horal,P. and Lindh,M.
TITLE Long-term mutation rates in the hepatitis B virus genome
J. Gen. Virol. 81 (Pt 1), 75-83 (2000)
MEDLINE 20109034
PUBMED 10640544
REFERENCE 2 (bases 1 to 3215)
Hannoun,C., Horal,P. and Lindh,M.
TITLE Direct Submission
Submitted (19-JAN-1999); Clinical Virology, Laboratory Medicine,
Guldhedsgatan 10B, Goteborg 413 46, Sweden
Location/Qualifiers

FEATURES
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AUTHORS	1 (bases 1 to 3215) Huang,W.J., Zhang,H.Y., Wang,Y.C., Wu,X., Gu,W.J., Ling,J.X. and Lan,H.Y.
TITLE	Direct Submission
JOURNAL	Submitted (31-JAN-2002) NO 2 Department of Viral Vaccines, National Institute for the Control of Pharmaceutical and Biological Products, Tiantan Xili 2#, Beijing, P.R. China
FEATURES	Location/Qualifiers

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Best Local Similarity 99.4%; Pred. No. 7.2e-187;
Matches 677; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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GenCore version 5.1.6
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SUMMARIES

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21	631.4	92.7	3183	1	Aaz29453 Hepatitis
22	631.4	92.7	3200	1	Aaz29453 Hepatitis
23	631.4	92.7	3200	1	Aaz29453 Hepatitis

24	631.4	92.7	3221	2	Aaz23281
25	631.4	92.7	3221	9	Add27773
26	631.4	92.7	3504	2	Aaz23281
27	631.4	92.7	3504	2	Aaz23281
28	631.4	92.7	4084	4	Aad14316
29	631.4	92.7	4084	4	Aad14316
30	631.4	92.7	5128	5	Aad06791
31	631.4	92.7	5459	5	Aad06792
32	631.4	92.7	5882	5	Aad06793
33	631.4	92.7	6371	2	Aaz23282
34	631.4	92.7	6371	2	Aaz23282
35	631.4	92.7	6375	2	Aaz23282
36	631.4	92.7	9325	2	Aaz23282
37	631.4	92.7	9859	2	Aaz23282
38	628.8	92.3	1355	1	Aan30059
39	628.4	92.3	678	3	Aac66340
40	628.4	92.3	678	4	Aaf21780
41	628.4	92.3	678	5	Aaf21780
42	628.4	92.3	678	6	Aab92880
43	628.4	92.3	678	6	Aab92880
44	628.2	92.2	681	7	Aab92880
45	628.2	92.2	687	1	Aan92275

ALIGNMENTS

RESULT 1
ID AAZ29453 standard; DNA; 3215 BP.

AC AAZ29453;

DT 06-AUG-2003 (revised)
DT 14-MAR-2000 (first entry)

DE Mutant hepatitis B viral genome.

KW HBIG; Hepatitis B immunoglobulin; HBV; Hepatitis B virus;

KW mutant major surface antigen; human hepatitis B viral genome;

KW human hepatitis B virus surface antigen- 'S'- 145 Singapore strain;

KW hepatocellular carcinoma; HBV infection; circular; cyclic; ds.

OS Hepatitis B virus.

PH Key Location/Qualifiers

FT CDS 1374..1835

FT /tag= d

FT /product= "Trans-activating X protein"

FT CDS 1814..2452

FT /tag= c

FT /product= "Core protein sequence"

FT mat_peptide 2307..3213

FT /tag= a

FT /transl_except= (pos:2595..2597 Glu)

FT /transl_except= (pos:2904..2906 Glu)

FT /note= "Partial sequence of DNA polymerase antigen"

FT mat_peptide 2848..3213

FT /tag= b

FT /note= "Partial human hepatitis B virus large antigen"

XX WO9966047-A1.

XX 23-DEC-1999.

XX 19-JUN-1998; 98WO-SG000045.

XX 19-JUN-1998; 98WO-SG000045.

XX (GOVE-) GOVERNMENT REPUBLIC SINGAPORE.

XX Ocn CJ, Lim GK, Leong AL, Zhao Y, Chen WN;

DR WPI; 2000-106103/09.
 DR P-PSDB; AAY44348; AAY44349, AAY44350, AAY44351.
 XX New vaccine-escape mutant of hepatitis B virus and related proteins,
 PT nucleic acids and antibodies, useful for diagnosis, prevention and
 PT treatment.
 XX Claim 3; Fig 3; 65pp; English.
 XX The present sequence encodes 4 overlapping reading frames of mutant human
 CC hepatitis B viral genome. This was isolated from a male, 11 year old
 CC Singaporean child which had received standard HBIG and HB vaccine and was
 CC infected with the mutated strain designated human hepatitis B virus
 CC surface antigen- 'S'-145 Singapore strain, a year later. This DNA is
 CC used for recombinant production of mutant major surface antigen and as a
 CC source of diagnostic oligonucleotides. The mutated major surface antigen
 CC is used to raise specific antibodies, to identify specific binding agents
 CC and, in vaccines or compositions for treatment or prevention of HBV
 CC infection and hepatocellular carcinoma. Antibodies are used in diagnosis
 CC or for screening donated body fluids or tissues. (Updated on 06-AUG-2003
 CC to correct OS field.)
 XX Sequence 3215 BP; 736 A; 852 C; 726 G; 901 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 681; DB 3; Length 3215;
 Best Local Similarity 100.0%; Pred. No. 4.3e-199;
 Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGAGAACATCGATCAGACTCTTAGAGCCCTGCTGCTGTATCAGCGGGGTTTTC 60
 Db 155 ATGGAGAACATCGATCAGACTCTTAGAGCCCTGCTGCTGTATCAGCGGGGTTTTC 214
 QY 61 TTGTTGCAAAATCTCAAAATACCGAGCTAGAGTCTGCTGGTGGACTTCTCTCAAT 120
 Db 215 TTGTTGCAAAATCTCAAAATACCGAGCTAGAGTCTGCTGGTGGACTTCTCTCAAT 274
 QY 121 TTCTAGGGGAAACCGGTTGCTGTGGCAAAATTCGAGTCCCAATCTCCAGTCA 180
 Db 275 TTCTAGGGGAAACCGGTTGCTGTGGCAAAATTCGAGTCCCAATCTCCAGTCA 334
 QY 181 TCACCAACCTGTGCTCCAAATTCCTGCTGTTATCGCTGGATGCTGCGGGTTT 240
 Db 335 TCACCAACCTGTGCTCCAAATTCCTGCTGTTATCGCTGGATGCTGCGGGTTT 394
 QY 241 ATCATCTTCTCTGCACTCTGCTGCTATGCTCTCTTCTTGTGTTCTTCTGCACT 300
 Db 395 ATCATCTTCTCTGCACTCTGCTGCTATGCTCTCTTCTTGTGTTCTTCTGCACT 454
 QY 301 CRAAGTATGTTGCGGTTTCTCTTAATTCAGGATCAACAACACGACCGGACCA 360
 Db 455 CRAAGTATGTTGCGGTTTCTCTTAATTCAGGATCAACAACACGACCGGACCA 514
 QY 361 TGCAAAACCTGCACAACTCTGCTCAAGAACTCTATGTTTCCCTCATGTTGCTGTACA 420
 Db 515 TGCAAAACCTGCACAACTCTGCTCAAGAACTCTATGTTTCCCTCATGTTGCTGTACA 574
 QY 421 AAACCTACGACGAAACTGCACTGTATTCGATCCCATCATCTTGGGCTTTCGCAAAA 480
 Db 575 AAACCTACGACGAAACTGCACTGTATTCGATCCCATCATCTTGGGCTTTCGCAAAA 634
 QY 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTACTAGTGCATTGTT 540
 Db 635 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTACTAGTGCATTGTT 694
 QY 541 CAGTGTGCTGAGGGCTTTCCGCCACTGCTGCTGCTTTCAGTTATAGATGATGGTTT 600
 Db 695 CAGTGTGCTGAGGGCTTTCCGCCACTGCTGCTGCTTTCAGTTATAGATGATGGTTT 754
 QY 601 TGGGGCCCAAGTCTGTACAACTCTTGGCTTTCAGTCCCTTATGCGCTGTACCAATTTCTTT 660
 Db 755 TGGGGCCCAAGTCTGTACAACTCTTGGCTTTCAGTCCCTTATGCGCTGTACCAATTTCTTT 814
 QY 661 TGTCTTTGGGTATACATTTAA 681

Db 815 TGTCTTTGGGTATACATTTAA 835
 RESULT 2
 AAQ98180
 ID AAQ98180 standard; DNA; 690 BP.
 XX
 AC AAQ98180;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 19-DEC-1995 (first entry)
 XX
 DE Hepatitis B virus surface antigen protein (HBsAg) isolate 2.
 XX
 KW Hepatitis B virus; surface antigen; envelope region; 'a' determinant; ss.
 XX
 OS Hepatitis B virus; isolate 2.
 XX
 FH Key Location/Qualifiers
 FT variation 368..376
 FT /*tag= a
 FT /label= insertion
 FT
 PN WO9521189-A1.
 XX
 PD 10-AUG-1995.
 XX
 PF 02-FEB-1995; 95WO-GB000208.
 XX
 PR 02-FEB-1994; 94GB-00001987.
 XX
 PA (UNLO) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.
 XX
 PI Karayiannis P, Thomas HC;
 XX
 DR WPI; 1995-283727/37.
 XX
 PT New mutant hepatitis B surface antigen - used for the detection
 XX prevention and treatment of hepatitis B infection.
 XX
 PS Claim 10; Fig 7; 39pp; English.
 XX
 CC Two Chinese patients with hepatitis were studied. Patient No. 1 was a 58
 CC year old male, with a 6 year history of non-A, non-B chronic hepatitis.
 CC HBV-DNA was found by PCR in the absence of HBsAg and other HBV markers at
 CC a time when the patient had cirrhosis. Patient No. 2 was a 23 year old
 CC woman from the south of China who on routine testing had a slightly
 CC elevated serum aminotransferase (ALT) level and was positive for HBsAg
 CC and HBeAg, but negative for both immunoglobulin (Ig) M and IgG anti-HBs.
 CC On follow-up she continued to be HBV-DNA positive and was also anti-HBc.
 CC positive but negative for HBsAg, HBeAg and anti-HBs. Both patients were
 CC negative for hepatitis C virus (HVC) and HVC-RNA. DNA was isolated from
 CC serum samples and used as a template for PCR amplification. Primers M3
 CC and 3C (see AAQ98187 & AAQ98188) were used to amplify the Pre-C and C
 CC regions. Direct sequencing of the PCR products was carried out using
 CC sequencing primers AAQ98181-Q98186. The S genes consist of 687 bp in
 CC isolate 1, 690 bp in isolate 2 and 681 bp in the wild types. The S
 CC nucleotide and AA sequences of the mutants were compared with a published
 CC sequence of the same subtype (adw) and also with a wild type strain from
 CC an HBeAg-positive carrier from the same region. Sequencing results
 CC revealed an insertion in the S gene. Inserted sequences encode two
 CC additional AAs (Arg-Ala) between codons 122 and 123 in isolate 1, and
 CC three additional AAs (Arg-Gly-Ala) between codons 123 and 124 in isolate
 CC 2. These insertions occur immediately before the 'a' determinant of
 CC HBsAg. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-
 CC 2003 to standardise OS field)
 XX
 SQ Sequence 690 BP; 140 A; 186 C; 145 G; 219 T; 0 U; 0 Other;
 Query Match 96.3%; Score 655.6; DB 2; Length 690;
 Best Local Similarity 98.1%; Pred. No. 1.5e-191;

QY 361 TGCAA-----AACCTGCACAACTCCTGCTCAAGGAACCTCTATGTTTCCCTCATGTCG 414
 Db 361 TGCAACGGGCAACCTGCACAACTCCTGCTCAAGGAACCTCTATGTTTCCCTCATGTCG 420
 QY 415 TGTAACAACTACGGAAGAGAACTGCACCTGTATTCCTCCATCCCATCATCTTTGGGCTTTC 474
 Db 421 TGTAACAACTACGGAAGAGAACTGCACCTGTATTCCTCCATCCCATCATCTTTGGGCTTTC 480
 QY 475 GCAAAATACCTATGGGAGTGGGCTCAGTCCGTTTCTTTGGCTCAGTTTACTAGTGCCA 534
 Db 481 GCAAAATACCTATGGGAGTGGGCTCAGTCCGTTTCTTTGGCTCAGTTTACTAGTGCCA 540
 QY 535 TTGTTCAGTGGTTCGAGGCTTTCCCTCCACCTGCTGCTGCTTTCAGTTATATGGATGATG 594
 Db 541 TTGTTCAGTGGTTCGAGGCTTTCCCTCCACCTGCTGCTGCTTTCAGTTATATGGATGATG 600
 QY 595 TGGTTTGGGGGCAAGTCTGTACAACTCTGAGTCCCTTTATGCGGCTGTACCAATT 654
 Db 601 TGGTTTGGGGGCAAGTCTGTACAACTCTGAGTCCCTTTATGCGGCTGTACCAATT 660
 QY 655 TTCTTTTGTCTTTGGGTATACATTAA 681
 Db 661 TTCTTTTGTCTTTGGGTATACATTAA 687

RESULT 4

AAZ88924
 ID AAZ88924 standard; DNA; 3220 BP.

XX AC AAZ88924;
 XX DT 06-AUG-2003 (revised)
 XX DT 26-MAY-2000 (first entry)

XX Hepatitis B virus genomic DNA fragment.

XX Detection; PCR; diagnosis; infection; ds.

XX Hepatitis B virus.

XX DE19835856-A1.

XX PN 17-FEB-2000.

XX PF 07-AUG-1998; 98DE-01035856.

XX PR 07-AUG-1998; 98DE-01035856.

XX PA (ROTH/) ROTH W K.

XX PA (DROS/) DROSTEN C.

XX PI Roth WK, Drosten C;

XX XX WPI; 2000-183936/17.

XX Oligonucleotide primers and probes, for the detection of hepatitis B
 PT virus, are used to amplify, by polymerase chain reaction, a section of
 PT the hepatitis B virus genome.

PS Disclosure; Page 8-11; 22pp; German.

XX This invention describes a novel method of detecting hepatitis B virus
 CC (HBV) in a sample which comprises exposing the sample to a polymerase
 CC chain reaction (PCR), where the PCR amplified DNA fragment corresponds to
 CC part of the HBV genome in the region of positions 242-482 of the HBV
 CC genome, counted from the single EcoRI cleavage site in the genome. The
 CC oligonucleotides and methods are useful for the detection of hepatitis B
 CC virus in samples. This is useful for the diagnosis of chronic hepatitis B
 CC infection. This sequence represents a fragment of the HBV genome
 CC described in the method of the invention. (Updated on 06-AUG-2003 to
 CC correct OS field.)

XX Sequence 3220 BP; 733 A; 862 C; 716 G; 909 T; 0 U; 0 Other;

Query Match 93.7%; Score 637.8; DB 3; Length 3220;
 Best Local Similarity 96.0%; Pred. No. 9.1e-186;
 Matches 654; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 ATGAGAAATCGCATCAGGACTCCTAGGACCCCTGCTCGTGTACAGGCGGGTTTTTC 60
 Db 156 ATGAGAAATCGCATCAGGACTCCTAGGACCCCTGCTCGTGTACAGGCGGGTTTTTC 215
 QY 61 TTGTTGCAAAATCCTCAATACCGCAGAGCTAGACTCGTGTGAGACTTCTCTCAAT 120
 Db 216 TTGTTGCAAAATCCTCAATACCGCAGAGCTAGACTCGTGTGAGACTTCTCTCAAT 275
 QY 121 TTTCTAGGGGAAACACCCGCTGTCTTTGGCCAAAATTCGCAGTCCCACTCCAATCAC 180
 Db 276 TTTCTAGGGGAAACACCCGCTGTCTTTGGCCAAAATTCGCAGTCCCACTCCAATCAC 335
 QY 181 TCACCAACTGTTGCTCTCCAAATTTGCTGTTATCGCTGGATGTCTCGGGCGTTTTT 240
 Db 336 TCACCAACTGTTGCTCTCCAAATTTGCTGTTATCGCTGGATGTCTCGGGCGTTTTT 395
 QY 241 ATCATCTTCTCTGCTGCTGCTATGCTCATCTTCTTGTGGTTCCTCTGGACTAT 300
 Db 396 ATCATCTTCTCTGCTGCTGCTATGCTCATCTTCTTGTGGTTCCTCTGGACTAT 455
 QY 301 CAAGGTATGTTCCCGTTTGTCTCTAATTCAGGATCAACAACACGACGACCGGACCA 360
 Db 456 CAAGGTATGTTCCCGTTTGTCTCTAATTCAGGATCAACAACACGACGACCGGACCA 515
 QY 361 TGCAAAACCTGCACAACTCCTGCTCAAGGAACCTCTATGTTTCCCTCATGCTGTGACA 420
 Db 516 TGCAAAACCTGCACAACTCCTGCTCAAGGAACCTCTATGTTTCCCTCATGCTGTGACA 575
 QY 421 AAACCTACGACAGAAACTGCACTGATTTCCCATCCCATCATCTTTGGGCTTTTCGCAAAA 480
 Db 576 AAACCTTCCGACGGAATACTGCCTGATTTCCCATCCCATCATCTTTGGGCTTTTCGCAAAA 635
 QY 481 TACCTATGGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCATTGTT 540
 Db 636 TTCTATGGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCATTGTT 695
 QY 541 CAGTGGTTCGTAGGGCTTTTCCCGACCTGCTGGCTTTTCACTTATATGATGATGTGGTTT 600
 Db 696 CAGTGGTTCGTAGGGCTTTTCCCGACCTGCTGGCTTTTCACTTATATGATGATGTGGTTT 755
 QY 601 TGGGGGCAAGTCTGTACAACTCTTGAGTCCCTTTTATGCCGCTGTACCAATTTCTTT 660
 Db 756 TGGGGGCAAGTCTGTACAACTCTTGAGTCCCTTTTATGCCGCTGTACCAATTTCTTT 815
 QY 661 TGTCTTTGGGTATACATTAA 681
 Db 816 TGTCTTTGGGTATACATTAA 836

RESULT 5

AAQ75318
 ID AAQ75318 standard; DNA; 684 BP.

XX AC AAQ75318;

XX DT 25-MAR-2003 (revised)

XX DT 22-SEP-1995 (first entry)

XX Mutant Hepatitis B virus nucleic acid sequence.

XX Hepatitis B virus; HBV, mutant; detection; surface antigen; HBsAg;
 XX detection; vaccine; diagnostic; prognosis; therapy; ss.

XX Hepatitis B virus.

XX Key Location/Qualifiers

XX FT misc_difference 185..187

XX /*tag= a

Db 1030 CAGTGGTTCGAGGGCTTCCCCCACTGTTGGCTTTCAGCTATATGATGATGAT 1089
Qy 601 TGGGGGCCAAGTCTGTACAAATCTTGAGTCCCTTTATGCGCTGTACCAATTTCTTT 660
Db 1090 TGGGGGCCAAGTCTGTACAGCATCGTGTGCTTTATACCGCTGTACCAATTTCTTT 1149
Qy 661 TGTCTTTTGGGTATACATTAA 681
Db 1150 TGTCTCTGGGTATACATTAA 1170

RESULT 8
AAN60152
ID AAN60152 standard; DNA; 681 BP.
XX AAN60152;
XX 25-MAR-2003 (revised)
DT 24-AUG-1991 (first entry)
XX Sequenc encoding adw type hepatitis B virus (HBV).
XX Vaccine; hepatitis B virus; antigen; ss.
XX Hepatitis B virus.

XX
XX Key Location/Qualifiers
XX CDS 1..681
XX /*tag= a
XX
XX EF1/5283-A.
XX
XX 26-MAR-1986.
XX 12-SEP-1985; 85EP-00111530.
XX 13-SEP-1984; 84JP-00193765.
XX (TAKE) TAKEDA CHEM IND LTD.
XX Kikuchi M, Fujisawa Y;
XX WPI; 1986-083075/13.
DR P-PSDB; AAP60223.

XX Recombinant DNA contg. gene for hepatitis B surface antigen - and
PT sequence complementary for 18S ribosomal RNA, and new yeast
PT transformants.
XX Disclosure; Fig 1; 29pp; English.

XX The pref. DNA coding for the surface antigen of adw type hepatitis B
CC virus is AAN60152. The recombinant DNA of the invention (see PT) is used
CC to transform yeast cells to produce HBsAg in quantities sufficient for
CC making vaccines. (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 681 BP; 139 A; 182 C; 142 G; 218 T; 0 U; 0 Other;

Query Match 92.7%; Score 631.4; DB 1; Length 681;
Best Local Similarity 95.4%; Pred. No. 4.2e-184;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 1 ATGGAGACATCGCATCAGGACCTCTAGGACCCCTCTCGTGTATACAGGGGGGTTTTC 60
Db 1 ATGGAGAACATCATCAGGATTCCTTAGGACCCCTCTCGTGTATACAGGGGGGTTTTC 60
Qy 61 TTGTTGACAAAATTCCTCACAATACCGCAGACTGTAGACTCGTGGTGGACTTCTCTCAAT 120
Db 61 TTGTTGACAGATTCCTCACAATACCGCAGACTGTAGACTCGTGGTGGACTTCTCTCAAT 120
Qy 121 TTCTAGGGGAAACCCCGTGTGTCTGGCCAAAATTCGAGTCCCAATCTCCAGTCAAC 180

Db 121 TTTCTAGGGGATCACCCGTGTCTTTGGCCAAAATTCGAGTCCCAACCTCCCAATCAC 180
Qy 181 TCACCAACCTGTTGTCTCCAAATTTGTCTGGTTATCGCTGGATGTTCTGCGCGTTTT 240
Db 181 TCACCAACCTGTTGTCTCCAAATTTGTCTGGTTATCGCTGGATGTTCTGCGCGTTTT 240
Qy 241 ATCATCTCTCTGCAFCCTGCTGTATGCTCATCTTCTTGTGTTCTTCTTGGACTAT 300
Db 241 ATCATATTCCTTTCATCTGCTGTATGCTCATCTTCTTATTTGGTCTTCTTGGATAT 300
Qy 301 CAAAGGTATGTTGCCGTTTGTCTCTAAATTCAGGATCAACAACAACAGCAGCGGACCA 360
Db 301 CAAAGGTATGTTGCCGTTTGTCTCTAAATTCAGGATCAACAACAACAGTACGGGACCA 360
Qy 361 TGCAAAACCTGCACAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 420
Db 361 TGCAAAACCTGCACAACTCTGCTCAAGGAACCTCTAAAGTTTCCCTCATGTTGCTGTACA 420
Qy 421 AAACCTACGGATGGAATTCACCTGTATCCCATCCATCGTCTGGGCTTTCGCAAAA 480
Db 421 AAACCTACGGATGGAATTCACCTGTATCCCATCCATCGTCTGGGCTTTCGCAAAA 480
Qy 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTTTGGCTCAGTTTACTAGTGCCATTTGTT 540
Db 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTTTGGCTCAGTTTACTAGTGCCATTTGTT 540
Qy 541 CAGTGGTTCGTAGGGCTTCCCACTGTCTGCTGCTTTCAGTTATATGATGATGCTGTT 600
Db 541 CAGTGGTTCGTAGGGCTTCCCACTGTCTGCTGCTTTCAGTTATATGATGATGCTGTT 600
Qy 601 TGGGGGCCAAGTCTGTATACAACTCTTGAGTCCCTTTATGCGCTGTATACCAATTTCTTT 660
Db 601 TGGGGGCCAAGTCTGTATACAACTCTTGAGTCCCTTTATGCGCTGTATACCAATTTCTTT 660
Qy 661 TGTCTTTGGGTATACATTAA 681
Db 661 TGTCTCTGGGTATACATTAA 681

RESULT 9
AAN80974
ID AAN80974 standard; DNA; 681 BP.
XX AAN80974;
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 21-JAN-1991 (first entry)
XX Sequence encoding S protein having hepatitis B virus (HBV) surface
XX antigen (HBsAg) activity.
XX DE antigen (HBsAg) activity.
XX KW Egg white lysozyme; hepatitis B virus (HBV) surface antigen (HBsAg);
KW Saccharomyces cerevisiae AH228/PGLD LP39-Rct;
KW Saccharomyces cerevisiae Liip39-Rct; Saccharomyces cerevisiae LP31-Rct;
KW protein secretion; ss.
XX Hepatitis B virus.
XX Key Location/Qualifiers
XX CDS 1..681
XX /*tag= a
XX EP288198-A.
XX 26-OCT-1988.
XX 13-APR-1988; 88EP-00303297.
XX 20-APR-1987; 87JP-00098265.
XX 12-OCT-1987; 87JP-00256885.
XX 18-APR-1988; 88JP-00095335.
XX

PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 XX Fujisawa Y, Imai S, Miyazaki T;
 XX
 XX WPI; 1988-301233/43.
 DR P-ESDB; RAP80417.
 XX
 XX
 XX Peptide(s) having hepatitis B surface antigenicity - used as vaccine for
 PT prevention of hepatitis B virus infection and in diagnostic kits.
 XX
 XX Disclosure; Fig 6; 31pp; English.
 XX
 XX A recombinant DNA which codes for a signal peptide which functions in a
 CC eukaryotic cell is bound to the 5'-terminus of a DNA coding for a peptide
 CC having hepatitis B virus (HBV) surface antigen (HBsAg) activity is
 CC claimed. The signal peptide may be a signal peptide of egg white
 CC lysozyme. The signal peptide - HBsAg DNA construct, which is claimed, is
 CC used to transform a eukaryotic cell, pref. a yeast cell, esp.
 CC Saccharomyces cerevisiae AH22R-/pGLD LP39-Rct, L11P39-Rct or LP31-Rct.
 CC The advantage is that peptides having HBsAg antigenicity are excreted
 CC outside the cells and easily purified. (Updated on 25-MAR-2003 to correct
 CC PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-
 CC AUG-2003 to correct OS field.)
 XX
 XX
 XX Sequence 681 BP; 139 A; 181 C; 143 G; 218 T; 0 U; 0 Other;
 SQ
 Query Match 92.7%; Score 631.4; DB 1; Length 681;
 Best Local Similarity 95.4%; Pred. No. 4.2e-184;
 Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
 QY 1 ATGAGAACATCGATCAGACTCTTAGAGCCCTGCTGCTGTTACAGCGGGGTTTTTC 60
 Db 1 ATGAGAACATCATCAGGATTCCTAGGACCCCTGCTGTTACAGCGGGGTTTTTC 60
 QY 61 TTGTTGACAAATCTTCAATACCGCAGAGTCTAGACTCGTGTTGAGTCTCTCAAT 120
 Db 61 TTGTTGACAGATCTTCAATACCGCAGAGTCTAGACTCGTGTTGAGTCTCTCAAT 120
 QY 121 TTCTAGGGGGAACACCGGTGTCTTGGCAAAATTCGAGTCCCAAAATCTCCAGTCAC 180
 Db 121 TTCTAGGGGGAACACCGGTGTCTTGGCAAAATTCGAGTCCCAAAATCTCCAGTCAC 180
 QY 181 TCACCAACCTGTCGCAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 420
 Db 181 TCACCAACCTGTCGCAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 420
 QY 421 AACCTTACCGACAGAACTGCACTGTATTCGATCCCATCATCTTGGCTTTGCGCAAAA 480
 Db 421 AACCTTACCGATGGAATGCACTGTATTCGATCCCATCATCTTGGCTTTGCGCAAAA 480
 QY 481 TACCTATGGAGTGGGCTCAGTCCGTTCTCTTGCTCAGTTTACTAGTGCCATTGTT 540
 Db 481 TACCTATGGAGTGGGCTCAGTCCGTTCTCTTGCTCAGTTTACTAGTGCCATTGTT 540
 QY 541 CAGTGGTTCGTAGGGCTTTCCGCCACTGTCCTGGCTTTTCACTATGATGATGTTT 600
 Db 541 CAGTGGTTCGTAGGGCTTTCCGCCACTGTCCTGGCTTTTCACTATGATGATGTTT 600
 QY 601 TGGGGGCCAAGTCTGTACAACTCTTGAGTCCCTTTATGCGCTGTACCAATTTCTTT 660
 Db 601 TGGGGGCCAAGTCTGTACAACTCTTGAGTCCCTTTATGCGCTGTACCAATTTCTTT 660

QY 661 TGCTTTGGGTATATACATTTAA 681
 Db 661 TGCTTTGGGTATATACATTTAA 681

RESULT 10

AAH19689
 ID AAH19689 standard; DNA; 681 BP.
 XX
 XX AC AAH19689;
 XX
 XX DT 20-JUL-2001 (first entry)
 XX
 XX DE DNA sequence used in the production of an HBV vaccine.
 XX
 XX KW Hepatitis B virus; HBV; HBV surface antigen; HBsAg; vaccine;
 XX gene expression; saccharomycetes; PCR primer; ss.
 XX OS Unidentified.
 XX
 XX PN CN1280011-A.
 XX
 XX PD 17-JAN-2001.
 XX
 XX PF 09-JUN-2000; 2000CN-00112328.
 XX
 XX PR 09-JUN-2000; 2000CN-00112328.
 XX
 XX PA (XING/) XING J.
 XX
 XX PI Xing J, Hou Y, Guo X;
 XX
 XX DR WPI; 2001-282453/30.
 XX
 XX PT Double expression process of producing hepatitis B virus vaccine.
 XX
 XX PS Disclosure; Page 2 (disclosure); 8pp; Chinese.
 XX

The present sequence is provided in a specification relating to a method for producing a vaccine. Two identical hepatitis B virus surface antigen (HBsAg) gene expressing units were cloned into an expression vector and then integrated into a saccharomycetes chromosome to raise the expression efficiency of the recombinant saccharomycetes. Hepatitis B virus strains may be identified by means of simple screening and a slow methanol metabolic cloning process

SQ Sequence 681 BP; 137 A; 182 C; 142 G; 220 T; 0 U; 0 Other;

Query Match 92.7%; Score 631.4; DB 4; Length 681;
 Best Local Similarity 95.4%; Pred. No. 4.2e-184;
 Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 ATGAGAACATCGATCAGACTCTTAGAGCCCTGCTGTTTACAGCGGGGTTTTTC 60
 Db 1 ATGAGAACATCATCAGGATTCCTAGGACCCCTGCTGTTTACAGCGGGGTTTTTC 60
 QY 61 TTGTTGACAAATCTTCAATACCGCAGAGTCTAGACTCGTGTTGAGTCTCTCAAT 120
 Db 61 TTGTTGACAAATCTTCAATACCGCAGAGTCTAGACTCGTGTTGAGTCTCTCAAT 120
 QY 121 TTCTAGGGGGAACACCGGTGTCTTGGCAAAATTCGAGTCCCAAAATCTCCAGTCAC 180
 Db 121 TTCTAGGGGGAATCTCCGTTGTCTTGGCAAAATTCGAGTCCCAAAATCTCCAGTCAC 180
 QY 181 TCACCAACCTGTTGCTCTCAATTTGCTGGTTATGCTGGATGTTCTGCGGCTTTT 240
 Db 181 TCACCAACCTGTTGCTCTCAATTTGCTGGTTATGCTGGATGTTCTGCGGCTTTT 240
 QY 241 ATCATCTTCTCTGTCATCTGCTGCTATGCCATCTTCTTGTGTTCTTCTGGAATAT 300
 Db 241 ATCATATCTTCTTTCATCTCTGCTGCTATGCCATCTTCTTGTGTTCTTCTGGAATAT 300

QY 301 CAAGGTATGTCGCCGTTGTCCTCTAATTCAGGATCAAAACAACAGCAGCGACCA 360
Db 301 CAAGGTATGTCGCCGTTGTCCTCTAATTCAGGATCAAAACAACAGCAGCGACCA 360
QY 361 TCGAAACCTGCAACCTCTCTCTCAAGAACTCTATGTTTCCCTCTATGTTGCTGTACA 420
Db 361 TCGAAACCTGCAACCTCTCTCTCAAGAACTCTATGTTTCCCTCTATGTTGCTGTACA 420
QY 421 AATCTACGGACAGAACTGCAACCTGATTCCTCCATCCCATCATCTTGGCTTTGCAAAA 480
Db 421 AATCTACGGACAGAACTGCAACCTGATTCCTCCATCCCATCATCTTGGCTTTGCAAAA 480
QY 481 TACCTATGGAGTGGGCTCTAGTCCGTTTCTCTCTGCTCAGTTTACTAGTGCATTGTT 540
Db 481 TACCTATGGAGTGGGCTCTAGTCCGTTTCTCTCTGCTCAGTTTACTAGTGCATTGTT 540
QY 541 CAGTGGTTCGTAGGCTTTCCGCACTGCTGGCTTTCAGTTATATGATGATGTTGTT 600
Db 541 CAGTGGTTCGTAGGCTTTCCGCACTGCTGGCTTTCAGTTATATGATGATGTTGTT 600
QY 601 TGGGGGCCAAGTCTGTACAACTCTGAGTCCCTTTATGCCCTCTGTATACCGCTGTACCAATTTCTTT 660
Db 601 TGGGGGCCAAGTCTGTACAACTCTGAGTCCCTTTATGCCCTCTGTATACCGCTGTACCAATTTCTTT 660
QY 661 TGTCTTTGGGTATACATTAA 681
Db 661 TGTCTTTGGGTATACATTAA 681

RESULT 11
ID AAN70247 standard; DNA; 690 BP.
XX AC
XX AC
XX AAN70247;
DT 24-OCT-2003 (revised)
DT 03-APR-1991 (first entry)
XX DE Hybrid sequence of Pichia pastoris regulatory region and hepatitis B
XX DE surface antigen coding region.
XX KW Hepatitis B virus antigen; vaccine; ss.
XX OS Pichia pastoris; and hepatitis B virus.
XX PN EP226846-A.
XX PD 01-JUL-1987.
XX PF 25-NOV-1986; 86EP-00116302.
XX PR 26-NOV-1985; 85US-00801713.
XX PHIP) PHILLIPS PETROLEUM CO.
XX Tschopp JF, Harpold MM, Gregg JM, Buckholz RG;
XX WPI; 1987-179248/26.
XX Yeast prodn. of hepatitis B surface antigen - with regulatory regions
XX responsive to methanol non-catabolite repressing carbon source or carbon
XX source starvation.
XX PS Claim 5; p21; 33pp; English.
XX The regulatory region is derived from the dihydroxyacetone synthase (DAS)
XX gene of Pichia pastoris, from the primary alcohol oxidase (AOXI) gene of
XX P. pastoris or from the p40 gene of P. pastoris. Using AAN70247, HBsAg
XX can be produced in high yields. (Updated on 24-OCT-2003 to standardise OS
XX field)
XX Sequence 690 BP; 139 A; 184 C; 145 G; 222 T; 0 U; 0 Other;

Query Match 92.7%; Score 631.4; DB 1; Length 690;
Best Local Similarity 95.4%; Pred. No. 4.2e-184;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1 ATGGAGAACATCGCATCAGCACTCCCTAGGACCCCTGCTGCTGTATACAGGCGGGTTTTC 60
Db 7 ATGGAGAACATCATCAGGATTCCTAGGACCCCTGCTGCTGTATACAGGCGGGTTTTC 66
QY 61 TTGTTGACAAAAATCCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
Db 67 TTGTTGACAAAGATCCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 126
QY 121 TTCTAGGGGGAACACCCGTTGCTTGGCCAAATTCGCGAGTCCGAAATCTCCAGTCAC 180
Db 127 TTCTAGGGGGAATCTCCCGTTGCTTGGCCAAATTCGCGAGTCCGAAATCTCCAGTCAC 186
QY 181 TCACCAACCTGTTGCTCTCCCAATTTGCTGGTATATCGCTGGATGTCTGCGGCGTTT 240
Db 187 TCACCAACCTGTTGCTCTCCCAATTTGCTGGTATATCGCTGGATGTCTGCGGCGTTT 246
QY 241 ATCATCTCTCTGCTGCTGCTGCTATGCTCATCTTCTTGTGTTCTTCTGGAATAT 300
Db 247 ATCATCTCTCTGCTGCTGCTGCTATGCTCATCTTCTTGTGTTCTTCTGGAATAT 306
QY 301 CARGGTATGTGCCGTTTGTCTCTAATTCAGGATCAACAACACAGCAGCGGACCA 360
Db 307 CARGGTATGTGCCGTTTGTCTCTAATTCAGGATCAACAACACAGTACGCGGACCA 366
QY 361 TGCAAAACCTGCACACTCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTGCTGTACA 420
Db 367 TGCAAAACCTGCACACTCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTGCTGTACA 426
QY 421 AAACCTAGGACAGAACTGCACTGCTGATTCCTCATCCATCCATCTGCGGTTTCGCAAAA 480
Db 427 AAACCTAGGATGGAAATGCACTGCTGATTCCTCATCCATCCATCTGCGGTTTCGCAAAA 486
QY 481 TACCTATGGAGTGGGCTCTAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCATTGTT 540
Db 487 TACCTATGGAGTGGGCTCTAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCATTGTT 546
QY 541 CAGTGGTTCGTAGGCTTTCCGCACTGCTGGCTTTCAGTTATATGATGATGTTGTT 600
Db 547 CAGTGGTTCGTAGGCTTTCCGCACTGCTGGCTTTCAGTTATATGATGATGTTGTT 606
QY 601 TGGGGGCCAAGTCTGTACAACTCTGAGTCCCTTTATGCCCTGTGTACCAATTTCTTT 660
Db 607 TGGGGGCCAAGTCTGTACAACTCTGAGTCCCTTTATGCCCTGTGTACCAATTTCTTT 666
QY 661 TGTCTTTGGGTATACATTAA 681
Db 667 TGTCTTTGGGTATACATTAA 687

RESULT 12
ID AAO11323 standard; DNA; 756 BP.
XX AC
XX AAO11323;
XX XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 10-JUN-1991 (first entry)
XX DE
DE RP135/HBsAg.
XX KW HIV; envelope; AIDS; ARC; hepatitis; fusion; vaccine; antibodies; ss.
XX OS Hepatitis B virus.
XX Synthetic.
XX Key Location/Qualifiers
XX CDS 1..75
XX PT /*tag= a

FT /label= bases 901-973 of HIV envelope
 FT /note= "BH10 serotype"
 FT 76..753
 FT /*tag= b
 FT /label= HBsAg gene

XX EP421626-A.
 XX
 XX 10-APR-1991.
 XX
 XX 17-SEP-1990; 90EP-00310108.
 XX
 XX 19-SEP-1989; 89US-00409180.
 PR 19-SEP-1989; 89US-00409190.
 XX
 XX (MERI) MERCK & CO INC.
 XX
 XX Kniskern PJ, Hagopian A, Burke P;
 XX WPI; 1991-103853/15.
 DR P-PSDB; AAR11495.
 XX
 PT Recombinant fusion polypeptide(s) of HIV envelope - for treatment or
 PT prophylaxis of AIDS, ARC and hepatitis before and after infection.
 XX
 XX Claim 1; Page 6; 26pp; English.
 XX
 CC HBV Dana (serotype adw) was cloned in pBR322 and, after modifica- tions,
 CC was ligated with a synthetic fragment of DNA encoding the RP135 ORF of
 CC HIV envelope protein, serotype BH10. The resulting plasmid,
 CC HIVR135/HBsAg, was used to express the recombinant fusion protein which
 CC can be used as an immunogen. See also AAQ11324. (Updated on 25-MAR-2003
 CC to correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)
 XX
 XX SQ Sequence 756 BP; 166 A; 194 C; 162 G; 234 T; 0 U; 0 Other;

Query Match 92.7%; Score 631.4; DB 2; Length 756;
 Best Local Similarity 95.4%; Pred. No. 4.4e-184;
 Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 ATGAGAAATCGCATCAGGACTCTTCAGGACCCCTGCTGTTTACAGCGGGGTTTTC 60
 DB 76 ATGAGAAATCATCATCAGGACTCTTCAGGACCCCTGCTGTTTACAGCGGGGTTTTC 135
 QY 61 TTGTTGACAAATCTCTCAATACCGGAGAGTCTAGACTCGTGTGGACTTCTCTCAAT 120
 DB 136 TTGTTGACAAATCTCTCAATACCGGAGAGTCTAGACTCGTGTGGACTTCTCTCAAT 195
 QY 121 TTCTAGGGGGAACACCGGTGTCTTGGCCAAATTCGAGTCCCAATCTCCAGTCAAC 180
 DB 196 TTCTAGGGGGAATCTCCGTTGTCTTGGCCAAATTCGAGTCCCAATCTCCAGTCAAC 255
 QY 181 TCACCAACCTGTGTCTCTCAATTTGCTGTTTATCGCTGGATGTGTGGCGGTTT 240
 DB 256 TCACCAACCTGTGTCTCTCAATTTGCTGTTTATCGCTGGATGTGTGGCGGTTT 315
 QY 241 ATCATCTTCTGTGATCTGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGAT 300
 DB 316 ATCATCTTCTGTGATCTGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGAT 375
 QY 301 CAAGTATGTTGCCGTTTGTCTCTTAATTCAGGATCAACCAACCAACCAACCAACCA 360
 DB 376 CAAGTATGTTGCCGTTTGTCTCTTAATTCAGGATCAACCAACCAACCAACCAACCA 435
 QY 361 TCGAAACCTGCACACTCTGCTCAAGAACTCTATGTTTCCCTCATGTTGCTGTACA 420
 DB 436 TCGAAACCTGCACACTCTGCTCAAGAACTCTATGTTTCCCTCATGTTGCTGTACA 495
 QY 421 AAACCTACGGACAGAAATCGACCTGTATTCATCCATCCCATCATCTTGGGCTTTCGCAAAA 480
 DB 496 AAACCTACGGATGGAATTCGACCTGTATTCATCCATCCCATCATCTTGGGCTTTCGCAAAA 555
 QY 481 TACCTATGGAGTGGGCTTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 540

DB 556 TACCTATGGAGTGGGCTTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 615
 QY 541 CAGTGTTCGTAGGGCTTTCCCCACACTGTCTGGCTTTTCAGTTATATGATGATGTTT 600
 DB 616 CAGTGTTCGTAGGGCTTTCCCCACACTGTCTGGCTTTTCAGTTATATGATGATGTTT 675
 QY 601 TGGGGCCCAAGTCTGTACCAACATCTTGAGTCCCTTTATGCGGCTGTACCAATTTCTTT 660
 DB 676 TGGGGCCCAAGTCTGTACCAACATCTTGAGTCCCTTTATGCGGCTGTACCAATTTCTTT 735
 QY 661 TGTCTTTGGGTATACATTAA 681
 DB 736 TGTCTTTGGGTATACATTAA 756

RESULT 13

AAQ10677
 ID AAQ10677 standard; DNA; 843 BP.
 XX
 AC AAQ10677;
 XX
 DT 25-MAR-2003 (revised)
 DT 29-APR-1991 (first entry)
 XX
 DE Modified hepatitis B virus large protein (III).
 XX
 KW Hepatitis B virus; large surface protein; L protein; myristilation;
 KW vaccines; ss.
 XX
 OS Hepatitis B virus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..123
 FT /*tag= a
 FT /label= pre-S1_region
 FT 124..162
 FT /*tag= b
 FT /label= pre-S2_region
 FT 163..843
 FT /*tag= c
 FT /label= S-protein

XX EP414374-A.

XX 27-FEB-1991.

XX 19-JUL-1990; 90EP-00307900.

XX 25-JUL-1989; 89US-00385342.

XX 03-AUG-1989; 89US-00389184.

XX (SMK) SMITHKLINE BIOLOGIC.

XX (COMB/) COMBERBACH M.

PI Comberbach M, Harford N, Cabazon T, Rutgers A, Voet P, Jacobs E;

PI Hollenberg CP, Janowicz ZA, Merckelbach AJ;

XX WPI; 1991-059585/09.

XX P-PSDB; AAR10850.

XX Modified hepatitis B virus large surface protein - has amino acid

XX sequence encoding L protein used in vaccine for treating or preventing

XX hepatitis B without side-effects.

XX Disclosure; Page 4-7; 79pp; English.

XX The modified protein comprises amino acids 12-52 (amino acid 13 is opt.

XX deleted), followed by 133-145, then 175-400 of the wild-type sequence.

XX This protein is devoid of the following properties: to function as a

XX substrate to yeast glycosylation enzymes; polymerised human serum albumin

XX binding capacity and protease sensitivity. The modified product may be

XX used alone or in a composite particle comprising at least two

CC polypeptides corresp. to all or part of a protein having the biological
CC activity of one of the hepatitis B surface antigens. The composite
CC particles are useful for preparing improved hepatitis B vaccines or for
CC treating of HBV. See also AAQ10677-79. (Updated on 25-MAR-2003 to correct
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 843 BP; 174 A; 229 C; 179 G; 261 T; 0 U; 0 Other;

Query Match 92.7%; Score 631.4; DB 2; Length 843;
Best Local Similarity 95.4%; Pred. No. 4.6e-184;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1 ATGGAGAACATCGCATCAGGACTCTAGGACCCCTGCTGTTACAGCGGGGTTTTTC 60
Db 163 ATGGAGAACATCAGATCAGGATTCCTAGGACCCCTGCTGTTACAGCGGGGTTTTTC 222
QY 61 TTGTTGACAAAATCCTCAATACCGAGAGCTAGACTGCTGTGTGAGACTTCTCAAT 120
Db 223 TTGTTGACAAAATCCTCAATACCGAGAGCTAGACTGCTGTGTGAGACTTCTCAAT 282
QY 121 TTTCTAGGGGACACCCGCTGCTTGGCCAAATTCGACATCCCAATCTCCAGTCAC 180
Db 283 TTTCTAGGGGATCACCCTGCTGCTTGGCCAAATTCGACATCCCAATCTCCAGTCAC 342
QY 181 TCACCAACCTGTGTCTCTCAATTTGCTGTTATCGTGGATGCTGCGGGTTTTT 240
Db 343 TCACCAACCTGTGTCTCTCAATTTGCTGTTATCGTGGATGCTGCGGGTTTTT 402
QY 241 ATCACTTCTCTGCACTGCTGCTATGCTCATCTTCTGTTCTTCTGCTGACTAT 300
Db 403 ATCATATTCCTTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 462
QY 301 CAAGGTATGTGCGCGTTTGTCTCTTAATTCAGGATCAACAAACAGCAGCGGACCA 360
Db 463 CAAGGTATGTGCGCGTTTGTCTCTTAATTCAGGATCAACAAACAGCAGCGGACCA 522
QY 361 TGCAAAACCTGCACAACTCCTGCTCAAGAACTCTATGTTTCCCTCATGTTGCTGTACA 420
Db 523 TGCAAAACCTGCACAACTCCTGCTCAAGAACTCTATGTTTCCCTCATGTTGCTGTACA 582
QY 421 AACCTACGACAGAACTGCACCTGATTCCTATCCATCCCATCTTTGGGCTTTTCGAAA 480
Db 583 AACCTACGACAGAACTGCACCTGATTCCTATCCATCCCATCTTTGGGCTTTTCGAAA 542
QY 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTGCTCAGTTTACTAGTGCATTTGTT 540
Db 643 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTGCTCAGTTTACTAGTGCATTTGTT 702
QY 541 CAGTGTTCGTAGGGCTTTCCCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 703 CAGTGTTCGTAGGGCTTTCCCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 762
QY 601 TGGGGGCCAAGTCTGTACAACTCTTGAAGTCCCTTTATGCGCTGTATACCAATTTTCTTT 660
Db 763 TGGGGGCCAAGTCTGTACAACTCTTGAAGTCCCTTTATGCGCTGTATACCAATTTTCTTT 822
QY 661 TGCTTTTGGGTATACATTTAA 681
Db 823 TGCTTTTGGGTATACATTTAA 843

RESULT 14
AAN93424
ID AAN93424 standard; DNA; 852 BP.
XX
AC AAN93424;
XX
AC
XX
DT 25-MAR-2003 (revised)
DT 05-APR-1990 (first entry)
XX
XX Sequence of hepatitis B virus preS2 sequence.
XX
KW Hepatitis B virus; preS2 protein; S protein; vaccine.

XX Hepatitis B virus.
OS
XX
XX Key Location/Qualifiers
FT CDS 7
FT /*tag= a
FT /note= "start of preS2 protein"
FT 172
FT /*tag= b
FT /note= "start of S protein"
XX
XX EP341746-A.
XX
XX 15-NOV-1989.
XX
XX 13-MAY-1988; 88US-00193714.
XX
XX 13-MAY-1988; 88US-00193714.
XX
XX (PHIP) PHILLIPS PETROLEUM CO.
XX (RESE) RESEARCH CORP TECHNOLOGIES INC.
XX
XX Thill GP;
XX
XX WPI; 1989-334102/46.
XX
XX Expression of hepatitis B S and preS2 proteins in methylotrophic yeast -
XX used to obtain antigenic hepatitis B virus particles in more vaccine-
XX effective form.
XX
XX Disclosure; Table 1; 36pp; English.
XX
XX An expression cassette contg. the preS2 gene, and an expression cassette
XX contg. the S gene are used to transform a methylotrophic yeast, to produce
XX antigenic HBV particles which combine the major S protein with the more
XX potentially antigenic preS2 protein. This particle is in a more effective
XX vaccine form. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
XX 25-MAR-2003 to correct PI field.)
XX
XX Sequence 852 BP; 175 A; 235 C; 182 G; 260 T; 0 U; 0 Other;
SQ
Query Match 92.7%; Score 631.4; DB 1; Length 852;
Best Local Similarity 95.4%; Pred. No. 4.7e-184;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1 ATGGAGAACATCGCATCAGGACTCTAGGACCCCTGCTGTTACAGCGGGGTTTTTC 60
Db 172 ATGGAGAACATCAGATCAGGATTCCTAGGACCCCTGCTGTTACAGCGGGGTTTTTC 231
QY 61 TTGTTGACAAAATCCTCAATACCGAGAGTCTAGACTGCTGTGAGACTTCTCTCAAT 120
Db 232 TTGTTGACAAAATCCTCAATACCGAGAGTCTAGACTGCTGTGAGACTTCTCTCAAT 291
QY 121 TTTCTAGGGGAAACACCGGTGCTTTGGCCAAAATTCGAGATCCCAATCTCCAGTCAC 180
Db 292 TTTCTAGGGGATCTCCCGTGTCTTTGGCCAAAATTCGAGATCCCAATCTCCAGTCAC 351
QY 181 TCACCAACCTGTGTCTCTCAATTTGCTGTTATCGTGGATGCTGCTGCGGGTTTTT 240
Db 352 TCACCAACCTGTGTCTCTCAATTTGCTGTTATCGTGGATGCTGCTGCGGGTTTTT 411
QY 241 ATCATCTTCTCTGTCATCTCTGCTATGCTGCTCAATTTCTTTGTTGTTCTTCTGAGCTAT 300
Db 412 ATCATATTTCTTCTTCTATCTCTGCTATGCTGCTCAATTTCTTTGTTGTTCTTCTGAGTAT 471
QY 301 CAGGTATGTTGCGCGTTTTGCTCTTAATTCAGGATCAACAAACAGCAGCGGACCA 360
Db 472 CAAGGTATGTTGCGCGTTTTGCTCTTAATTCAGGATCAACAAACAGCAGCGGACCA 531
QY 361 TGCAAAACCTGCACAACTCCTGCTCAGAGAACTCTATGTTTCCCTCATGTTGCTGTACA 420
Db 532 TGCAAAACCTGCACAACTCCTGCTCAGAGAACTCTATGTTTCCCTCATGTTGCTGTACA 591

QY 421 AACCTACGACAGAACTGCACCTGTATCCCATCCCATCATCTTGGGCTTTTCGAAAA 480
 DB 592 AACCTACGATGGAATTCACCTGTATCCCATCCCATCGTCTGGGCTTTTCGAAAA 651
 QY 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTTTGGCTCAGTTTACTAGTGCATTTGTT 540
 DB 652 TACCTATGGAGTGGGCTCAGTCCGTTTCTTTGGCTCAGTTTACTAGTGCATTTGTT 711
 QY 541 CAGTGGTTCTAGGCTTTCCGCCACTGTCTGGCTTTTCACTATATGGATGATGTTT 600
 DB 712 CAGTGGTTCTAGGCTTTCCGCCACTGTCTGGCTTTTCACTATATGGATGATGTTT 771
 QY 601 TGGGGCCAAAGTCTGTACAGATCGTGGAGTCCCTTTATACCGCTGTTACCAATTTTCTTT 660
 DB 772 TGGGGCCAAAGTCTGTACAGATCGTGGAGTCCCTTTATACCGCTGTTACCAATTTTCTTT 831
 QY 661 TGTCTTTGGGTATACATTTAA 681
 DB 832 TGTCTTTGGGTATACATTTAA 852

RESULT 15

AAN91823

ID AAN91823 standard; DNA; 859 BP.

AC AAN91823;

XX 22-MAR-1990 (first entry)

DT Pre-S2 structural gene.

DE Antigen.

XX Hepatitis B virus.

XX Key Location/Qualifiers

XX mat_peptide 7..852

FT /tag= a

FT /note= "pre-S2 protein"

FT mat_peptide 172..852

FT /tag= b

FT /note= "S protein"

FT

XX EP339567-A.

XX

XX 02-NOV-1989.

XX 25-APR-1989; 89EP-00107457.

XX 25-APR-1988; 88US-00186421.

XX (PHIP) PHILLIPS PETROLEUM CO.

XX Thill GP;

XX WPI; 1989-317441/44.

XX P-PSDB; AAP93168.

XX Expression of hepatitis B Pres2 protein - in methylotrophic yeast, e.g.

XX Fichla pastoris.

XX Disclosure; Page 5-6; 22pp; English.

XX Pres2 is present in HBV viral coat protein with S and pres1. In the

XX patent it is used recombinantly to produce antigenic particles for

XX vaccine

XX

SQ Sequence 859 BP; 178 A; 238 C; 182 G; 261 T; 0 U; 0 Other;

Query Match 92.7%; Score 631.4; DB 1; Length 859;

Best Local Similarity 95.4%; Pred. No. 4.7e-184;

Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 ATGGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTCGTGTACAGGCGGGTTC 60
 DB 172 ATGGAGAACATCAGATCCTAGGACCCCTGCTCGTGTACAGGCGGGTTC 231
 QY 61 TTGTTGACAAAATCTCTACAAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
 DB 232 TTGTTGACAGAACTCTACAAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 291
 QY 121 TTTCTAGGGGAAACACCGGTGTCTTTGGCCAAAATTCGAGTCCGAAATCTCCAGTCAC 180
 DB 292 TTTCTAGGGGATCTCCCGGTGTCTTTGGCCAAAATTCGAGTCCGAAATCTCCAGTCAC 351
 QY 181 TCACCAACCTCTCTCTCCCAATTTGCTGGTGTATGGCTGGATGTCTGCGGCGTTT 240
 DB 352 TCACCAACCTCTCTCTCCCAATTTGCTGGTGTATGGCTGGATGTCTGCGGCGTTT 411
 QY 241 ATCATCT 300
 DB 412 ATCATCT 471
 QY 301 CAAGTATGTTGCCCGTTTGTCTCTAAATTCAGGATCAACAAACACGACACGACCA 360
 DB 472 CAAGTATGTTGCCCGTTTGTCTCTAAATTCAGGATCAACAAACACGACACGACCA 531
 QY 361 TGCAAAACCTGACAACTCTCTCTCAAGGAACTCTATGTTTCCCTCATGTTCTGTGACA 420
 DB 532 TGCAAAACCTGACAACTCTCTCTCAAGGAACTCTATGTTTCCCTCATGTTCTGTGACA 591
 QY 421 AARCTACGGACAGAACTGCACCTGTATTCCTCATCCATCCATCTTGGGCTTTTCGCAAA 480
 DB 592 AARCTACGGATGGAATTTGCACCTGTATTCCTCATCCATCCATCTTGGGCTTTTCGCAAA 651
 QY 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 540
 DB 652 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 711
 QY 541 CAGTGGTTCGTAGGGCTTTCCCCACCTGCTGGCTTTCAGTTATATGGATGATGTTT 600
 DB 712 CAGTGGTTCGTAGGGCTTTCCCCACCTGCTGGCTTTCAGTTATATGGATGATGTTT 771
 QY 601 TGGGGCCAAAGTCTGTACAAACATCTTGAGTCCCTTTTATGCCGCTGTATCCCAATTTTCTTT 660
 DB 772 TGGGGCCAAAGTCTGTACAAACATCTTGAGTCCCTTTTATGCCGCTGTATCCCAATTTTCTTT 831
 QY 661 TGTCTTTGGGTATACATTTAA 681
 DB 832 TGTCTTTGGGTATACATTTAA 852

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Job time : 377 secs

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OM nucleic - nucleic search, using sw model

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Searched: 682709 seqs, 277475446 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	669.8	98.4	681	2	US-08-500-914A-7
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3	655.6	96.3	690	2	US-08-500-914A-8
4	652.2	95.8	687	2	US-08-500-914A-6
5	634.8	93.2	684	1	US-08-447-591-1
6	634.8	93.2	684	1	US-08-450-943-1
7	634.8	93.2	684	1	US-08-059-031-1
8	634.8	93.2	684	2	US-08-450-942-1
9	634.8	92.7	684	5	PCT-US94-05090-1
10	631.4	92.7	893	2	US-08-500-914A-1
11	631.4	92.7	3220	6	5196194-15
12	631.4	92.7	3221	2	US-08-715-808-1
13	631.4	92.7	3504	2	US-08-760-797A-2
14	631.4	92.7	3504	2	US-08-760-797A-4
15	631.4	92.7	3504	3	US-08-932-929B-2
16	631.4	92.7	3504	2	US-08-932-929B-4
17	631.4	92.7	6371	2	US-08-715-808-5
18	631.4	92.7	6371	2	US-08-715-808-12
19	631.4	92.7	6375	2	US-08-715-808-14
20	631.4	92.7	9325	2	US-08-715-808-2
21	631.4	92.7	9859	2	US-08-715-808-6
22	629.8	92.5	3220	6	5196194-11
23	626.6	92.0	7463	2	US-08-715-808-13
24	621.8	91.3	846	4	US-09-247-890-11
25	621.8	91.3	846	4	US-09-724-969-11
26	621.8	91.3	846	4	US-09-724-852-11
27	621.8	91.3	3182	4	US-08-890-735C-1

28	621.8	91.3	3182	4	US-10-104-966-14
29	621.8	91.3	5618	3	US-08-799-569-1
30	621.8	91.3	5618	4	US-09-570-546-1
31	621.8	91.3	5618	4	US-09-146-072A-1
32	618.6	90.9	801	4	US-09-311-784A-15
33	618.6	90.8	1201	1	US-08-105-483-218
34	618.6	90.8	1201	1	US-08-709-209-218
35	618.6	90.8	1201	1	US-08-458-101-218
36	618.6	90.8	1285	1	US-08-105-483-215
37	618.6	90.8	1285	1	US-08-709-209-215
38	618.6	90.8	1285	1	US-08-458-101-215
39	617	90.6	681	4	US-09-471-573A-1
40	617	90.6	681	5	PCT-US96-10602-13
41	615.6	90.4	678	3	US-08-075-520A-26
42	615.6	90.4	817	1	US-08-378-011A-4
43	615.6	90.4	822	3	US-08-075-520A-14
44	615.6	90.4	845	1	US-08-378-011A-2
45	615.4	90.4	846	6	5164485-1

ALIGNMENTS

RESULT 1
US-08-500-914A-7
; Sequence 7, Application US/08500914A
; Patent No. 5856084
; GENERAL INFORMATION:
; APPLICANT: KARAVIANNIS, PETER
; APPLICANT: THOMAS, HOWARD C.
; TITLE OF INVENTION: HEPATITIS B VACCINE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/500.914A
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 1208-17
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 681 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-500-914A-7

Query Match 98.4%; Score 669.8; DB 2; Length 681;
Best Local Similarity 99.0%; Pred. No. 1.1e-200;
Matches 674; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY	1	ATGGAGACATCGCATCAGGACTCTAGGACCCCTGCTCGTGTACAGCGGGGTTTTTC	60
Db	1	ATGGAGACATCGCATCAGGACTCTAGGACCCCTGCTCGTGTACAGCGGGGTTTTTC	60
QY	61	TTGTTGACAAAATCCTCACAAATACCGCAGAGTCTAGACTCGTGTGGAGCTTCTCTCAAT	120

Db 61 TTGTTGACAAAATCCTCACAATACACAGAGCTAGACTCGTGGTGGACTTCTCTCAAT 120
Qy 121 TTTCTAGGGGAAACACCGGTGTGTCTTGGCAAAAATTCGAGTCCCAAAATCTCAGTAC 180
Db 121 TTTCTAGGGGAAACACCGGTGTGTCTTGGCAAAAATTCGAGTCCCAAAATCTCAGTAC 180
Qy 181 TCACCAACTGTTCTCTCAATTTGCTCTTAATTCAGGATCAACAACACGACCGGACCA 240
Db 181 TCACCAACTGTTCTCTCAATTTGCTCTTAATTCAGGATCAACAACACGACCGGACCA 240
Qy 241 ATCATCTTCTCTCAATTTGCTCTTAATTCAGGATCAACAACACGACCGGACCA 300
Db 241 ATCATCTTCTCTCAATTTGCTCTTAATTCAGGATCAACAACACGACCGGACCA 300
Qy 301 CAAGGTATGTTGGCCGTTTGTCTTAATTCAGGATCAACAACACGACCGGACCA 360
Db 301 CAAGGTATGTTGGCCGTTTGTCTTAATTCAGGATCAACAACACGACCGGACCA 360
Qy 361 TGCAAAACCTGCAACACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACA 420
Db 361 TGCAAAACCTGCAACACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACA 420
Qy 421 AAACCTAGGACAGAACTGCTGATTTCCCATCCCATCATCTTGGGCTTTCGCAAA 480
Db 421 AAACCTAGGACAGAACTGCTGATTTCCCATCCCATCATCTTGGGCTTTCGCAAA 480
Qy 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTTGGCTCAGTTTACTAGTGCCATTTGTT 540
Db 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTTGGCTCAGTTTACTAGTGCCATTTGTT 540
Qy 541 CAGTGGTTCGTAGGGCTTTCCCACTGCTGCTGCTTTCAGTTATAGGATGATGCTTT 600
Db 541 CAGTGGTTCGTAGGGCTTTCCCACTGCTGCTGCTTTCAGTTATAGGATGATGCTTT 600
Qy 601 TGGGGGCAAGTCTGTACAACATCTTGAGTCCCTTTATGCGGCTGTTACCAATTTCTTT 660
Db 601 TGGGGGCAAGTCTGTACAACATCTTGAGTCCCTTTATGCGGCTGTTACCAATTTCTTT 660
Qy 661 TGTCTTTGGGTATACATTTAA 681
Db 661 TGTCTTTGGGTATACATTTAA 681

RESULT 2

US-08-500-914A-9
; Sequence 9, Application US/08500914A
; Patent No. 5856084
; GENERAL INFORMATION:
; APPLICANT: KARAYIANNIS, PETER
; APPLICANT: THOMAS, HOWARD C.
; TITLE OF INVENTION: HEPATITIS B VACCINE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/500, 914A
; APPLICATION NUMBER: US/08/500, 914A
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHELL, LEONARD C.
; REGISTRATION NUMBER: 29, 009
; REFERENCE/DOCKET NUMBER: 1208-17

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 681 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-500-914A-9

Query Match 98.4%; Score 669.8; DB 2; Length 681;
Best Local Similarity 99.0%; Pred. No. 1.1e-200;
Matches 674; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ATGGAGACATCGCATCAGGACTCTAGGACCCCTGCTCGTGTACAGGGGGGTTTTC 60
Db 1 ATGGAGACATCGCATCAGGACTCTAGGACCCCTGCTCGTGTACAGGGGGGTTTTC 60
Qy 61 TTGTTGACAAAAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTTCTCAAT 120
Db 61 TTGTTGACAAAAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTTCTCAAT 120
Qy 121 TTTCTAGGGGAAACACCGGTGTGTCTTGGCCAAAATTCGAGTCCCAAAATCTCAGTAC 180
Db 121 TTTCTAGGGGAAACACCGGTGTGTCTTGGCCAAAATTCGAGTCCCAAAATCTCAGTAC 180
Qy 181 TCACCAACTGTTGCTCTCAATTTGCTCTTAATTCAGGATCAACAACACGACCGGACCA 240
Db 181 TCACCAACTGTTGCTCTCAATTTGCTCTTAATTCAGGATCAACAACACGACCGGACCA 240
Qy 241 ATCATCTTCTCTCAATTTGCTCTTAATTCAGGATCAACAACACGACCGGACCA 300
Db 241 ATCATCTTCTCTCAATTTGCTCTTAATTCAGGATCAACAACACGACCGGACCA 300
Qy 301 CAAGGTATGTTGGCCGTTTGTCTTAATTCAGGATCAACAACACGACCGGACCA 360
Db 301 CAAGGTATGTTGGCCGTTTGTCTTAATTCAGGATCAACAACACGACCGGACCA 360
Qy 361 TGCAAAACCTGCAACACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACA 420
Db 361 TGCAAAACCTGCAACACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACA 420
Qy 421 AAACCTAGGACAGAACTGCTGATTTCCCATCCCATCATCTTGGGCTTTCGCAAA 480
Db 421 AAACCTAGGACAGAACTGCTGATTTCCCATCCCATCATCTTGGGCTTTCGCAAA 480
Qy 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTTGGCTCAGTTTACTAGTGCCATTTGTT 540
Db 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTTGGCTCAGTTTACTAGTGCCATTTGTT 540
Qy 541 CAGTGGTTCGTAGGGCTTTCCCACTGCTGCTGCTTTCAGTTATAGGATGATGCTTT 600
Db 541 CAGTGGTTCGTAGGGCTTTCCCACTGCTGCTGCTTTCAGTTATAGGATGATGCTTT 600
Qy 601 TGGGGGCAAGTCTGTACAACATCTTGAGTCCCTTTATGCGGCTGTTACCAATTTCTTT 660
Db 601 TGGGGGCAAGTCTGTACAACATCTTGAGTCCCTTTATGCGGCTGTTACCAATTTCTTT 660
Qy 661 TGTCTTTGGGTATACATTTAA 681
Db 661 TGTCTTTGGGTATACATTTAA 681

RESULT 3

US-08-500-914A-8
; Sequence 8, Application US/08500914A
; Patent No. 5856084
; GENERAL INFORMATION:
; APPLICANT: KARAYIANNIS, PETER
; APPLICANT: THOMAS, HOWARD C.
; TITLE OF INVENTION: HEPATITIS B VACCINE

APPLICANT: SOLOMON, LARRY R
TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR
DETECTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: SOLOMON, LARRY R
FILING DATE: US/08/450,943
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5347.US.01
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..684
US-08-450-943-1

Query Match 93.2%; Score 634.8; DB 1; Length 684;
Best Local Similarity 96.6%; Pred. No. 1.1e-189;
Matches 661; Conservative 0; Mismatches 17; Indels 6; Gaps 1;

QY 1 ATGAGAACATCCATCAGAGCTCTAGGACCCCTCTCGTGTACAGCGGGGTTTTC 60
Db 1 ATGAGAACACCATCAGAGCTCTAGGACCCCTCTCGTGTACAGCGGGGTTTTC 60

QY 61 TTCTTCACAAATCTCAATACCGCAGCTAGACTCGTGTGGACTTCTCTCAAT 120
Db 61 TTCTTCACAAATCTCAATACCGCAGCTAGACTCGTGTGGACTTCTCTCAAT 120

QY 121 TTCTAGGGGGAACACCCGTGTCTTGGCCAAATTCGACGTCCTCCAGTCA 180
Db 121 TTCTAGGGGGAACACCCGTGTCTTGGCCAAATTCGACGTCCTCCAGTCA 180

QY 181 TCACCAACCTGTGTCTTCAATTTGCTGGTTATCGTGGATGTCTGGGGGTTT 240
Db 181 TCACCAACCTGTGTCTTCAATTTGCTGGTTATCGTGGATGTCTGGGGGTTT 240

QY 241 ATCATCTTCTCTGCACTCTGCTGCTATCTCTTGTGTGTCTTCTGGAAT 300
Db 241 ATCATCTTCTCTGCACTCTGCTGCTATCTCTTGTGTGTCTTCTGGAAT 300

QY 301 CAAGGTATGTGCGCGTTGTCTCTAATTCAGGATCAACAAACGACCGGACCA 360
Db 301 CAAGGTATGTGCGCGTTGTCTCTAATTCAGGATCAACAAACGACCGGACCA 360

QY 361 TG-----CAAACTCGCAACTCTGCTCAAGGACCTCTATGTTCCCTCATGTCG 414
Db 361 TGAGGAACACAACTCGCAGATCTCTGCTCAAGGACCTCTATGTTCCCTCATGTCG 420

QY 415 TGTACAAACCTACGACAGAACTGCACCTGTAATCCCATCCCATCATCTTGGGCTTTC 474
Db 415 TGTACAAACCTACGACAGAACTGCACCTGTAATCCCATCCCATCATCTTGGGCTTTC 480

Db 421 TGTACAAACCTACGACAGAACTGCACCTGTAATCCCATCCCATCATCTTGGGCTTTC 480
QY 475 GCAAAATACCTATGGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCCA 534
Db 481 GCAAAATTCCTATGGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCCA 540
QY 535 TTCTTTCAGTGGTTTCGTAGGCTTTTCCCCACCTGCTCGGCTTTCAGTTATATGATGATG 594
Db 541 TTCTTTCAGTGGTTTCGTAGGCTTTTCCCCACCTGCTCGGCTTTCAGTTATATGATGATG 600
QY 595 TGGTTTGGGGGCAAGCTCTGTACAACTCTGAGTCCCTTTATGCGCTGTACCAATT 654
Db 601 TGGTATTGGGGGCAAGCTCTGTACAACTCTGAGTCCCTTTATGCGCTGTACCAATT 660
QY 655 TTCTTTCAGTGGTTTCGTAGGCTTTTCCCCACCTGCTCGGCTTTCAGTTATATGATGATG 678
Db 661 TTCTTTCAGTGGTTTCGTAGGCTTTTCCCCACCTGCTCGGCTTTCAGTTATATGATGATG 684

RESULT 7
US-08-059-031-1
Sequence 1, Application US/08059031
Patent No. 5595739
GENERAL INFORMATION:
APPLICANT: CARMAN, WILLIAM
APPLICANT: DECKER, RICHARD H
APPLICANT: WALLACE, LESLEY
APPLICANT: MIMMS, LARRY T
APPLICANT: SOLOMON, LARRY R
TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/059,031
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5347.US.01
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..684
US-08-059-031-1

Query Match 93.2%; Score 634.8; DB 1; Length 684;
Best Local Similarity 96.6%; Pred. No. 1.1e-189;
Matches 661; Conservative 0; Mismatches 17; Indels 6; Gaps 1;

QY 1 ATGAGAACATCCATCAGAGCTCTAGGACCCCTCTCGTGTACAGCGGGGTTTTC 60
Db 1 ATGAGAACACCATCAGAGCTCTAGGACCCCTCTCGTGTACAGCGGGGTTTTC 60

RESULT 9
PCT-US94-05090-1
; Sequence 1, Application PC/TUS9405090
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLACE, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05090
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..684
PCT-US94-05090-1

Query Match 93.2%; Score 634.8; DB 5; Length 684;
Best Local Similarity 96.6%; Pred. No. 1.1e-189;
Matches 661; Conservative 0; Mismatches 17; Indels 6; Gaps 1;
QY 1 ATGGAGAACATCGCATCAGACGACCTCTAGGACCCCTGCTGTGTACAGCGGGGTTTTC 60
DB 1 ATGGAGAACACCATCAGACGACCTCTAGGACCCCTGCTGTGTACAGCGGGGTTTTC 60
QY 61 TTGTTGACAAAATCTCAATATCCGACAGTCTAGACTCGTGTGGACTTCTCTCAAT 120
DB 61 TTGTTGACAAAATCTCAATATCCGACAGTCTAGACTCGTGTGGACTTCTCTCAAT 120
QY 121 TTTCTAGGGGGAACACCGGTGTCTTGGCCAAAATTCGAGTCCCAATCTCCAGTAC 180
DB 121 TTTCTAGGGGGAACACCGGTGTCTTGGCCAAAATTCGAGTCCCAATCTCCAGTAC 180
QY 181 TCACCAACCTGTGTCTCTCAATTTGCTGTGTTATCGTGGATGTCTCGCGGCTTTT 240
DB 181 TCACCAACCTGTGTCTCTCAATTTGCTGTGTTATCGTGGATGTCTCGCGGCTTTT 240
QY 241 ATCATCTTCTCTGCAATCTGCTGCTATGCTCATCTTCTGTGTTTCTTCTGACTAT 300
DB 241 ATCATCTTCTCTGCAATCTGCTGCTATGCTCATCTTCTGTGTTTCTTCTGACTAT 300
QY 301 CRAAGTATGTCGCGGTTGTCTCTCAATTCAGGATCAACACACACGACCGGACCA 360
DB 301 CRAAGTATGTCGCGGTTGTCTCTCAATTCAGGATCAACACACACGACCGGACCA 360

QY 361 TG-----CAAAACCTGCACAACTCCCTGCTCAAGGAACCTCTATGTTTCCTCATGTTGC 414
DB 361 TGCAGGAACACAACTGCACGACTCCCTGCTCAAGGAACCTCTATGTTTCCTCATGTTGC 420
QY 415 TGTACAAAACCTACGGACAGAACTGCACCTGTATTCCTCCATCCCATCATCTTGGGCTTTC 474
DB 421 TGTACAAAACCTACGGACAGAACTGCACCTGTATTCCTCCATCCCATCATCTTGGGCTTTC 480
QY 475 GCAAAATACCTATGAGAGTGGGCTCAGTCCGTTTCTTCTGGCTCAGTTTACTAGTGCCA 534
DB 481 GCAAAATTCCTATGAGAGTGGGCTCAGTCCGTTTCTTCTGGCTCAGTTTACTAGTGCCA 540
QY 535 TTTCTTTCAGTGGTTCGTAGGGCTTTCCCACTGTCTGGCTTTCCAGTTATATGATGATG 594
DB 541 TTTCTTTCAGTGGTTCGTAGGGCTTTCCCACTGTCTGGCTTTCCAGTTATATGATGATG 600
QY 595 TGGTTTTGGGGGCCAAGTCTGTACAACTCTTGAGTCCCTTTATGCGCGCTGTACCAATT 654
DB 601 TGGTATTGGGGGCCAAGTCTGTACAACTCTTGAGTCCCTTTATGCGCGCTGTACCAATT 660
QY 655 TTCTTTTGTCTTTGGGTATACATT 678
DB 661 TTCTATTGTCTTTGGGTATACATT 684
RESULT 10
US-08-500-914A-1
; Sequence 1, Application US/08500914A
; Patent No. 5856084
; GENERAL INFORMATION:
; APPLICANT: KARAYIANIS, PETER
; APPLICANT: THOMAS, HOWARD C.
; TITLE OF INVENTION: HEPATITIS B VACCINE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/500,914A
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 1208-17
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 893 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-500-914A-1
Query Match 92.7%; Score 631.4; DB 2; Length 893;
Best Local Similarity 95.4%; Pred. No. 1.5e-188;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1 ATGGAGACATCGCATCAGGACTCCTAGGACCCCTGCTGTGTACAGCGGGGTTTTC 60

Db 129 ATGAGAACATCATCAGGATTCCTAGGACCCCTGCTGTGTATCAGGGGGTTTTTC 188
QY 61 TTGTTGACAAATAATCTCTCAATAACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
Db 189 TTGTTGACAAATAATCTCTCAATAACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 248
QY 121 TTCTTAGGGGGAACACCGGTGTCTTGGCCAAATTCGAGTCCCAATCTCCAGTCA 180
Db 249 TTCTTAGGGGGAATCTCCGGTGTCTTGGCCAAATTCGAGTCCCAATCTCCAGTCA 308
QY 181 TCACCAACCTGTTGTCTCTCAATTTGCTGTTATCGCTGGATGTCTGGGGCGTTTT 240
Db 309 TCACCAACCTGTTGTCTCTCAATTTGCTGTTATCGCTGGATGTCTGGGGCGTTTT 368
QY 241 ATCATCTTCTCTGCACTCTGCTATGCTCATCTCTTCTTGGTCTTCTTGGACTAT 300
Db 369 ATCATATTCCTCTCTCATCTGCTGCTATGCTCATCTCTTCTTGGTCTTCTTGGACTAT 428
QY 301 CAAGGTATGTTGGCCGTTTGTCTCTTAATTCAGGATCAACAACACGACCGGACCA 360
Db 429 CAAGGTATGTTGGCCGTTTGTCTCTTAATTCAGGATCAACAACACGACCGGACCA 488
QY 361 TGAACAACTGCACTCTGCTCAAGAACTCTATGTTTCCCTCATGTTTCTGCTGATA 420
Db 489 TGAACAACTGCACTCTGCTCAAGAACTCTATGTTTCCCTCATGTTTCTGCTGATA 548
QY 421 AAACCTACGACAGAACTGCACTGTTATTCATCCATCCATCTTGGGCTTTCGCAAAA 480
Db 549 AAACCTACGAGTGAATGCACTGTTATTCATCCATCCATCTTGGGCTTTCGCAAAA 608
QY 481 TACCTATGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 540
Db 609 TACCTATGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 668
QY 541 CAGTGGTTCGTAGGGCTTCCCACTGCTGCTTTCAGTTATATGAGTATGAGTGGTT 600
Db 669 CAGTGGTTCGTAGGGCTTCCCACTGCTGCTTTCAGTTATATGAGTATGAGTGGTT 728
QY 601 TGGGGCCAAAGTCTGTACAGATCGTGGTCCCTTTATGCGCTGTATACCAATTTCTTT 660
Db 729 TGGGGCCAAAGTCTGTACAGATCGTGGTCCCTTTATGCGCTGTATACCAATTTCTTT 788
QY 661 TGTCTTTGGGTATACATTTAA 681
Db 789 TGTCTCTGGGTATACATTTAA 809

RESULT 11
5196194-15
; Patent No. 5196194
; APPLICANT: RUTTER, WILLIAM J.; GOODMAN, HOWARD M.
; TITLE OF INVENTION: VACCINES CONTAINING HEPATITIS B S-PROTEIN
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/679,621
; FILING DATE: 7-DEC-1984
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 513,055
; FILING DATE: 12-JUL-1983
; APPLICATION NUMBER: 107,267
; FILING DATE: 21-DEC-1979
; APPLICATION NUMBER: 41,909
; FILING DATE: 24-MAY-1979
; SEQ ID NO:15:
; LENGTH: 3220
5196194-15

Query Match 92.7%; Score 631.4; DB 6; Length 3220;
Best Local Similarity 95.4%; Pred. No. 3e-188;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1 ATGAGAACATCATCAGGATTCCTAGGACCCCTGCTGTGTATCAGGGGGTTTTTC 60

Db 1564 ATGAGAACATCATCAGGATTCCTAGGACCCCTGCTGTGTATCAGGGGGTTTTTC 1623
QY 61 TTGTTGACAAATAATCTCTCAATAACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
Db 1624 TTGTTGACAAATAATCTCTCAATAACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 1683
QY 121 TTCTTAGGGGGAACACCGGTGTCTTGGCCAAATTCGAGTCCCAATCTCCAGTCA 180
Db 1684 TTCTTAGGGGGAATCTCCGGTGTCTTGGCCAAATTCGAGTCCCAATCTCCAGTCA 1743
QY 181 TCACCAACCTGTTGTCTCTCAATTTGCTGTTATCGCTGGATGTCTGGGGCGTTTT 240
Db 1744 TCACCAACCTGTTGTCTCTCAATTTGCTGTTATCGCTGGATGTCTGGGGCGTTTT 1803
QY 241 ATCATCTTCTCTGCACTCTGCTATGCTCATCTCTTCTTGGTCTTCTTGGACTAT 300
Db 1804 ATCATATTCCTCTCTCATCTGCTGCTATGCTCATCTCTTCTTGGTCTTCTTGGACTAT 1863
QY 301 CAAGGTATGTTGGCCGTTTGTCTCTTAATTCAGGATCAACAACACGACCGGACCA 360
Db 1864 CAAGGTATGTTGGCCGTTTGTCTCTTAATTCAGGATCAACAACACGACCGGACCA 1923
QY 361 TGAACAACTGCACTCTGCTCAAGAACTCTATGTTTCCCTCATGTTTCTGCTGATA 420
Db 1924 TGAACAACTGCACTCTGCTCAAGAACTCTATGTTTCCCTCATGTTTCTGCTGATA 1983
QY 421 AAACCTACGACAGAACTGCACTGTTATTCATCCATCCATCTTGGGCTTTCGCAAAA 480
Db 1984 AAACCTACGAGTGAATGCACTGTTATTCATCCATCCATCTTGGGCTTTCGCAAAA 2043
QY 481 TACCTATGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 540
Db 2044 TACCTATGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 2103
QY 541 CAGTGGTTCGTAGGGCTTCCCACTGCTGCTTTCAGTTATATGAGTATGAGTGGTT 600
Db 2104 CAGTGGTTCGTAGGGCTTCCCACTGCTGCTTTCAGTTATATGAGTATGAGTGGTT 2163
QY 601 TGGGGCCAAAGTCTGTACAGATCGTGGTCCCTTTATGCGCTGTATACCAATTTCTTT 660
Db 2164 TGGGGCCAAAGTCTGTACAGATCGTGGTCCCTTTATGCGCTGTATACCAATTTCTTT 2223
QY 661 TGTCTTTGGGTATACATTTAA 681
Db 2224 TGTCTCTGGGTATACATTTAA 2244

RESULT 12
US-08-715-808-1
; Sequence 1, Application US/08715808
; Patent No. 5981274
; GENERAL INFORMATION:
; APPLICANT: Tyrrell, D. Lorne J.
; APPLICANT: Chaisomchit, Sumonta
; APPLICANT: Chang, Lung-Ji
; TITLE OF INVENTION: Recombinant Hepatitis Virus Vectors
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/715,808
; FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: CHANG-02441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3221 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-715-808-1

Query Match 92.7%; Score 631.4; DB 2; Length 3221;
Best Local Similarity 95.4%; Pred. No. 3e-188;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY	1	ATGAGAAATCGATCCATCAGGACTCTAGGACCCCTGCTGTTAGAGCCCTGCTGTTAGAGCCGGGTTTTC	60
DB	157	ATGAGAAATCATCATCAGGATTCCTAGGACCCCTGCTGTTAGAGCCGGGTTTTC	216
QY	61	TTGTTGACAAAATCTCAATACCCGAGAGTCTAGACTCGTGTGGGACTTCTCTCAAT	120
DB	217	TTGTTGACAAAATCTCAATACCCGAGAGTCTAGACTCGTGTGGGACTTCTCTCAAT	276
QY	121	TTTCTAGGGGACACCCGTTGCTGTGGCCAAATTCGACGTCCTCAATCTCCAGTAC	180
DB	277	TTTCTAGGGGAGTCTCCCGTGTCTGTGGCCAAATTCGACGTCCTCAATCTCCAGTAC	336
QY	181	TCACCAACCTGTTGCTCTCCAAATTTGCTGTTATCGCTGATGTCTCGCGGCTTT	240
DB	337	TCACCAACCTGTTGCTCTCCAAATTTGCTGTTATCGCTGATGTCTCGCGGCTTT	396
QY	241	ATCATCTCTCTGATCTCTGCTGCTATGCTCATCTTCTGTTCTTCTGACTAT	300
DB	397	ATCATATCTCTCTGATCTCTGCTGCTATGCTCATCTTCTGTTCTTCTGACTAT	456
QY	301	CAAGGTATGTTGCCGTTTCTCTCTAAATTCAGGATCAACAACACCGACCGGACCA	360
DB	457	CAAGGTATGTTGCCGTTTCTCTCTAAATTCAGGATCAACAACACCGACCGGACCA	516
QY	361	TGCAAAACCTGCAAACTCTCTGCTCAAGGAACTCTATGTTCCCTCATGTTCTGTACA	420
DB	517	TGCAAAACCTGCAAACTCTCTGCTCAAGGAACTCTATGTTCCCTCATGTTCTGTACA	576
QY	421	AAACCTACGACAGAACTGCACTGTTATTCCTATCCCATCCATCTTGGGCTTTTCGAAA	480
DB	577	AAACCTACGACAGAACTGCACTGTTATTCCTATCCCATCCATCTTGGGCTTTTCGAAA	636
QY	481	TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCATTTGT	540
DB	637	TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCATTTGT	696
QY	541	CAGTGTTCGTAGGGCTTTCCCGCAGTCTGCTGGCTTTCAGTTATATGATGATGTTT	600
DB	697	CAGTGTTCGTAGGGCTTTCCCGCAGTCTGCTGGCTTTCAGTTATATGATGATGTTT	756
QY	601	TGGGGGCAAGTCTGTACAACTCTTGAGTCCCTTTATGCGGCTGTATACCAATTTCTTT	660
DB	757	TGGGGGCAAGTCTGTACAACTCTTGAGTCCCTTTATGCGGCTGTATACCAATTTCTTT	816
QY	661	TGCTTTGGGTATACATTTAA	681
DB	817	TGCTTTGGGTATACATTTAA	837

RESULT 13
US-08-760-797A-2
; Sequence 2, Application US/08760797A

Patent No. 5928902
GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBSAG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,797A
FILING DATE: 04-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: B45015-1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-760-797A-2

Query Match 92.7%; Score 631.4; DB 2; Length 3504;
Best Local Similarity 95.4%; Pred. No. 3.1e-188;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY	1	ATGAGAAATCGATCCATCAGGACTCTAGGACCCCTGCTGTTAGAGCCGGGTTTTC	60
DB	1653	ATGAGAAATCATCATCAGGATTCCTAGGACCCCTGCTGTTAGAGCCGGGTTTTC	1712
QY	61	TTGTTGACAAAATCTCAATACCCGAGAGTCTAGACTCGTGTGGGACTTCTCTCAAT	120
DB	1713	TTGTTGACAAAATCTCAATACCCGAGAGTCTAGACTCGTGTGGGACTTCTCTCAAT	1772
QY	121	TTTCTAGGGGACACCCGTTGCTGTGGCCAAATTCGACGTCCTCAATCTCCAGTAC	180
DB	1773	TTTCTAGGGGATCACCCTGTTGCTGTGGCCAAATTCGACGTCCTCAATCTCCAGTAC	1832
QY	181	TCACCAACCTGTTGCTCTCCAAATTTGCTGTTATCGCTGATGTCTCGCGGCTTT	240
DB	1833	TACCAACCTCTCTGCTCTCCAAATTTGCTGTTATCGCTGATGTCTCGCGGCTTT	1892
QY	241	ATCATCTCTCTCTGATCTCTGCTGCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCT	300
DB	1893	ATCATATCTCTCTCTGATCTCTGCTGCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1952
QY	301	CAAGGTATGTTGCCGTTTCTCTCTAAATTCAGGATCAACAACACCGACCGGACCA	360
DB	1953	CAAGGTATGTTGCCGTTTCTCTCTAAATTCAGGATCAACAACACCGACCGGACCA	2012
QY	361	TGCAAAACCTGCAAACTCTCTCAAGGAACTCTATGTTTCCCTCATGTTTGTGTACA	420
DB	2013	TGCAAAACCTGCAAACTCTCTCAAGGAACTCTATGTTTCCCTCATGTTTGTGTACA	2072

QY 421 AACCTAGGACAGAACTGACCTGTATTCCCATCCCATCACTCTGGGCTTCGCAAAA 480
DB 2073 AAACCTAGGATGAAATGACCTGTATTCCCATCCCATCGTCTGGGCTTCGCAAAA 2132
QY 481 TACCTATGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCCATTGTT 540
DB 2133 TACCTATGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCCATTGTT 2192
QY 541 CAGTGGTTCGTAGGCTTTCCCTCCACTGCTGCTGCTTTTCACTATATGATGATGTTT 600
DB 2193 CAGTGGTTCGTAGGCTTTCCCTCCACTGCTGCTGCTTTTCACTATATGATGATGTTT 2252
QY 601 TGGGGGCCAAGTCTGTACAACTCTGAGTCCCTTTTATGCGGCTGTTTACCAATTTCTTT 660
DB 2253 TGGGGGCCAAGTCTGTACAACTCTGAGTCCCTTTTATGCGGCTGTTTACCAATTTCTTT 2312
QY 661 TGTCTTTGGGTATACATTAA 681
DB 2313 TGTCTCTGGGTATACATTAA 2333

RESULT 14

US-08-760-797A-4
; Sequence 4, Application US/08760797A
; Patent No. 5928902
; GENERAL INFORMATION:
; APPLICANT: De Wilde, Michel
; APPLICANT: Cohen, Joseph
; TITLE OF INVENTION: Hybrid Protein Between CS
; TITLE OF INVENTION: Hybrid Protein Between CS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,797A
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/442,612
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: B45015-1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3504 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-760-797A-4

Query Match 92.7%; Score 631.4; DB 2; Length 3504;
Best Local Similarity 95.4%; Pred. No. 3.1e-188;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 ATCGAGAACTCCATCAGACTCTTAGGACCCCTGCTGTATACAGCGGGGTTTTTC 60

DB 1653 ATGGAGAACATCACATCAGGATCTCTAGGACCCCTGCTCGTGTACAGCGGGGTTTTTC 1712
QY 61 TTGTTGACAAAATCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
DB 1713 TTGTTGACAAAATCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 1772
QY 121 TTTCTAGGGGGAACACCGTGTCTTGGCCAAAATTCGCAATCCCAATCTCCAGTCAAC 180
DB 1773 TTTCTAGGGGGAACACCGTGTCTTGGCCAAAATTCGCAATCCCAATCTCCAGTCAAC 1832
QY 181 TCACCAACTGTTGTCCTCCAAATTTGCTGCTGTTATCGCTGGAATGTGTCGCGCGTTTT 240
DB 1833 TCACCAACTGTCCTGCTCCAAATTTGCTGCTGTTATCGCTGGAATGTGTCGCGCGTTTT 1892
QY 241 ATCATCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 1893 ATCATCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1952
QY 301 CAAGGTATGTTGCCCGTTTGTCTCTAATTCAGGATCAACAACAACAGCAGCGGACCA 360
DB 1953 CAAGGTATGTTGCCCGTTTGTCTCTAATTCAGGATCAACAACAACAGCAGCGGACCA 2012
QY 361 TGCAAAACCTGCACAACTCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 420
DB 2013 TGCAAAACCTGCACAACTCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 2072
QY 421 AAACCTACGGACAGAACTGTCACCTGCTATTCCTCATCCATCCATCTTGGGCTTTCGCAAAA 480
DB 2073 AAACCTACGGATGGAATGCACTGCTATTCCTCATCCATCCATCTTGGGCTTTCGCAAAA 2132
QY 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTTCTTGGCTCAGTTTACTAGTGCCATTGTT 540
DB 2133 TACCTATGGAGTGGGCTCAGTCCGTTTCTTCTTGGCTCAGTTTACTAGTGCCATTGTT 2192
QY 541 CAGTGGTTCGTAGGCTTTCCCTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 2193 CAGTGGTTCGTAGGCTTTCCCTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2252
QY 601 TGGGGGCCAAGTCTGTACAACTCTGAGTCCCTTTTATGCGGCTGTTTACCAATTTCTTT 660
DB 2253 TGGGGGCCAAGTCTGTACAACTCTGAGTCCCTTTTATGCGGCTGTTTACCAATTTCTTT 2312
QY 661 TGTCTTTGGGTATACATTAA 681
DB 2313 TGTCTCTGGGTATACATTAA 2333

RESULT 15

US-08-932-929B-2
; Sequence 2, Application US/08932929B
; Patent No. 6169171
; GENERAL INFORMATION:
; APPLICANT: De Wilde, Michel
; APPLICANT: Cohen, Joseph
; TITLE OF INVENTION: Hybrid Protein Between CS
; TITLE OF INVENTION: Hybrid Protein Between CS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/932,929B
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,797
; FILING DATE: 04-DEC-1996
; APPLICATION NUMBER: 08/442,612
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: B45015-1FWC2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3504 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-932-929B-2

Query Match 92.7%; Score 631.4; DB 3; Length 3504;
Best Local Similarity 95.4%; Pred. No. 3.1e-188;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1 ATGGAGAACATCGCATCAGACTCCTAGACCCCTCTGCTGTACAGGGGGGTTTTTC 50
Db 1653 ATGGAGAACATCATCAGGATTCCTAGGACCCCTCTGCTGTACAGGGGGGTTTTTC 1712
QY 61 TTGTTGACAAAATCCTCAATACCGCAGAGCTAGACTCGTGGTGGACTTCTCTCAAT 120
Db 1713 TTGTTGACAGATCCTCAATACCGCAGAGCTAGACTCGTGGTGGACTTCTCTCAAT 1772
QY 121 TTTCTAGGGGGACACCCGTTGTCTTGGCCAAAATTCGGAGTCCCAATCTCCAGTCA 180
Db 1773 TTTCTAGGGGGATCACCCGTTGTCTTGGCCAAAATTCGGAGTCCCAATCTCCATCAC 1832
QY 181 TCACCAACCTGTGCTCTCAATTTGTCCTGTTATCGCTGGATGTCTGGGGCGTTTT 240
Db 1833 TCACCAACCTCTCTCTCAATTTGTCCTGTTATCGCTGGATGTCTGGGGCGTTTT 1892
QY 241 ATCATCTTCTCTGCACTCTGCTGCTATGCTCATCTTCTTGTGGTTCTCTGGACTAT 300
Db 1893 ATCATATTCCTCTTCACTCTGCTGCTATGCTCATCTTCTTATGGTTCTCTGGATTAT 1952
QY 301 CAAGGTATGTGGCGTTGCTCTTAATTCAGGATCAACACACCGACCGGACCA 360
Db 1953 CAAGGTATGTGGCGTTGCTCTTAATTCAGGATCAACACACCGACCGGACCA 2012
QY 361 TGCAAAACCTGCACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACA 420
Db 2013 TGCAAAACCTGCACGACTCCTGCTCAAGGCACTCTATGTTCCCTCATGTTGCTGTACA 2072
QY 421 AAACCTACGGACAGAAACTGCACTGATTTCCCATCCCATCATCTTGGGCTTTCGCAAAA 480
Db 2073 AAACCTACGGATGGAATTCACCTGATTTCCCATCCCATCATCTTGGGCTTTCGCAAAA 2132
QY 481 TACCTATGGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCCATTGTT 540
Db 2133 TACCTATGGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCCATTGTT 2192
QY 541 CAGTGGTTCGTAGGGCTTTCCCACTGCTGCTGCTTCACTTATATGATGATGTTGTT 600
Db 2193 CAGTGGTTCGTAGGGCTTTCCCACTGCTGCTGCTTCACTTATATGATGATGTTGTT 2252
QY 601 TGGGGGCCAAGTCTGTACACACTTCAGTCCCTTATGCGCTGTATCCAAATTTCTTT 660
Db 2253 TGGGGGCCAAGTCTGTACACACTTCAGTCCCTTATGCGCTGTATCCAAATTTCTTT 2312
QY 661 TGCTTTGGGTATACATTTAA 681
Db 2313 TGCTCTGGGTATACATTTAA 2333

Search completed: July 26, 2004, 15:26:48
Job time : 81 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 14:45:15 ; Search time 410 Seconds

(without alignments)
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3216467 seqs, 2444149694 residues

Total number of hits satisfying chosen parameters: 6432934

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
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14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
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16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
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18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	663.4	97.4	3215	13	US-10-453-792-284
5	639.4	93.9	3221	13	US-10-453-792-283
6	632.6	92.9	1365	16	US-10-365-620-33
7	632.6	92.9	2037	16	US-10-365-620-28
8	632.6	92.9	2037	16	US-10-365-620-31
9	631.4	92.7	1696	15	US-10-267-922-15
10	631.4	92.7	3200	13	US-10-453-792-280
11	631.4	92.7	3221	13	US-10-453-792-279
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13	631.4	92.7	4496	10	US-09-781-891D-22
14	629.8	92.5	3182	13	US-10-453-792-304

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16 628.2 92.2 690 9 US-09-821-877-7
17 628.2 92.2 3221 10 US-09-848-616-133
18 628.2 92.2 3221 15 US-10-050-902-133
19 628.2 92.2 3221 15 US-10-050-898-133
20 626.6 92.0 3212 13 US-10-453-792-310
21 626.6 92.0 3221 13 US-10-453-792-281
22 625 91.8 3182 13 US-10-453-792-303
23 625 91.8 3182 13 US-10-453-792-307
24 623.4 91.5 690 9 US-09-821-877-6
25 623.4 91.5 1181 9 US-09-821-877-1
26 623.4 91.5 3182 13 US-10-453-792-302
27 623.4 91.5 3215 13 US-10-453-792-299
28 621.8 91.3 846 9 US-09-247-890-11
29 621.8 91.3 846 16 US-10-393-317-11
30 621.8 91.3 3161 13 US-10-453-792-301
31 621.8 91.3 3182 9 US-09-929-955-14
32 621.8 91.3 3182 14 US-10-104-966-14
33 621.8 91.3 3182 17 US-10-719-619-14
34 621.8 91.3 3212 13 US-10-453-792-309
35 621.8 91.3 5618 15 US-10-142-358-1
36 621.8 91.3 8007 9 US-09-837-297-3
37 621.8 91.3 8717 9 US-09-837-297-4
38 620.2 91.1 3221 13 US-10-453-792-282
39 618.8 90.9 801 13 US-10-371-525-15
40 618.8 90.9 801 16 US-10-371-069-15
41 618.8 90.9 801 16 US-10-371-645-15
42 618.8 90.9 801 16 US-10-371-260-15
43 618.6 90.8 3182 13 US-10-453-792-308
44 617 90.6 681 9 US-09-812-862-13
45 617 90.6 681 17 US-10-335-774-1

ALIGNMENTS

RESULT 1

US-10-453-792-287

; Sequence 287, Application US/10453792

; Publication No. US20040029110A1

; GENERAL INFORMATION:

; APPLICANT: STUYVER, LIEVEN

; ROSSAU, RUDI

; MAERTENS, GEERT

; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV

; NUMBER OF SEQUENCES: 313

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHVE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION NUMBER:

; APPLICATION NUMBER: US/10/453,792

; FILING DATE: 04-Jun-2003

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/155,885A

; FILING DATE: 08-Oct-1998

; APPLICATION NUMBER: PCT/EP97/02002

; FILING DATE: 21-APR-1997

; APPLICATION NUMBER: EP 96870053.4

; FILING DATE: 19-APR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: SADOFF, B.J.

; REGISTRATION NUMBER: 36,663

; REFERENCE/DOCKET NUMBER: 2551-5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 287:
SEQUENCE CHARACTERISTICS:
LENGTH: 3215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 287:
US-10-453-792-287

Query Match 98.4%; Score 669.8; DB 13; Length 3215;
Best Local Similarity 99.3%; Pred. No. 2.7e-209;
Matches 676; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTGTTACAGCGGGTTTTTC 60
DB 157 ATGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTGTTACAGCGGGTTTTTC 216

QY 61 TTGTTGACAAAATCCTCAATACGACGAGTCTAGCTCGGTGGGACTTCTCTCAAT 120
DB 217 TTGTTGACAAAATCCTCAATACGACGAGTCTAGCTCGGTGGGACTTCTCTCAAT 276

QY 121 TTTCTAGGGGAAACACCGGTGTGTCTTGGCCAAAATTCGACGTCCTCAATCTCAGTCA 180
DB 277 TTTCTAGGGGAAACACCGGTGTGTCTTGGCCAAAATTCGACGTCCTCAATCTCAGTCA 336

QY 181 TCACCAACCTGTTCTCTCAATTTGCTCGGTATCGCTGGATGTCTCGCGCGTTTT 240
DB 337 TCACCAACCTGTTCTCTCAATTTGCTCGGTATCGCTGGATGTCTCGCGCGTTTT 396

QY 241 ATCATCTCTCTGATCCTGCTGATGCTCATCTCTCTGTTGGTCTCTCTGGACTAT 300
DB 397 ATCATCTCTCTGATCCTGCTGATGCTCATCTCTCTGTTGGTCTCTCTGGACTAT 456

QY 301 CAAGTATGTTGCCCGTTTTGCTCTTAATTCAGGATCAACAAACAGCAGCAGCACCA 360
DB 301 CAAGTATGTTGCCCGTTTTGCTCTTAATTCAGGATCAACAAACAGCAGCAGCACCA 360

QY 421 AAACCTACGACGAAACTGCACTGATATCCCATCCCATCTCTCTGCTTGGCTTTGCAAAA 480
DB 577 AAACCTACGACGAAACTGCACTGATATCCCATCCCATCTCTCTGCTTGGCTTTGCAAAA 636

QY 481 TACCTATGGAGTGGGCTCAGTCCGTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 637 TACCTATGGAGTGGGCTCAGTCCGTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 696

QY 541 CAGTGGTTCGTAGGGCTTTCCCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 697 CAGTGGTTCGTAGGGCTTTCCCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 756

QY 601 TGGGGGCAAGTCTGACACATCTTGGTCCCTTTATGCGCGTGTATCAATTTCTTTT 660
DB 757 TGGGGGCAAGTCTGACACATCTTGGTCCCTTTATGCGCGTGTATCAATTTCTTTT 816

QY 661 TGTCTTTTGGGTATACATTTAA 681
DB 817 TGTCTTTGGGTATACATTTAA 837

RESULT 2

US-10-453-792-285

; Sequence 285, Application US/10453792

; Publication No. US20040029110A1

; GENERAL INFORMATION:

APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-Apr-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 285:
SEQUENCE CHARACTERISTICS:
LENGTH: 3215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 285:
US-10-453-792-285

Query Match 98.4%; Score 669.8; DB 13; Length 3215;
Best Local Similarity 99.0%; Pred. No. 3.1e-208;
Matches 674; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTGTTTACAGCGGGTTTTTC 60
DB 157 ATGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTGTTTACAGCGGGTTTTTC 216

QY 61 TTGTTGACAAAATCCTCAATACCGACGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
DB 217 TTGTTGACAAAATCCTCAATACCGACGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 276

QY 121 TTTCTAGGGGAAACACCGGTGTGTCTTGGCCAAAATTCGACGTCCTCAATCTCAGTCA 180
DB 277 TTTCTAGGGGAAACACCGGTGTGTCTTGGCCAAAATTCGACGTCCTCAATCTCAGTCA 336

QY 181 TCACCAACCTGTTCTCTCAATTTGCTCGGTATCGCTGGATGTCTCGCGCGTTTT 240
DB 337 TCACCAACCTGTTCTCTCAATTTGCTCGGTATCGCTGGATGTCTCGCGCGTTTT 396

QY 241 ATCATCTCTCTGATCCTGCTGATGCTCATCTCTCTGTTGGTCTCTCTGGACTAT 300
DB 397 ATCATCTCTCTGATCCTGCTGATGCTCATCTCTCTGTTGGTCTCTCTGGACTAT 456

QY 301 CAAGTATGTTGCCCGTTTTGCTCTTAATTCAGGATCAACAAACAGCAGCAGCACCA 360
DB 301 CAAGTATGTTGCCCGTTTTGCTCTTAATTCAGGATCAACAAACAGCAGCAGCACCA 360

Db 457 CRAAGTATGTCGCCGTTGTCCTCTAATCCAGGATCATCAACACGACGACCGACCA 516
QY 361 TGCAAACTCGACAACTCCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 420
Db 517 TGCAAACTCGACGACTCCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 576
QY 421 AAACCTACGACAGAACTGACCTGTATTCCTATCCCATCCATCATCTGGCTTTCCCAAAA 480
Db 577 AAACCTACGACGAGAACTGACCTGTATTCCTATCCCATCCATCATCTGGCTTTCCCAAAA 636
QY 481 TACCTATGGAGTGGGCTTCAGTCCGTTTCTCTTGGCTCAGTCTTACTAGTGCCATTGTT 540
Db 637 TACCTATGGAGTGGGCTTCAGTCCGTTTCTCTTGGCTCAGTCTTACTAGTGCCATTGTT 696
QY 541 CAGTGTTCGTAGGCTTTCCCTCCACTGCTGCTTCTAGTGTATGATGATGATGATGATGAT 600
Db 697 CAGTGTTCGTAGGCTTTCCCTCCACTGCTGCTTCTAGTGTATGATGATGATGATGATGAT 756
QY 601 TGGGGCCCAAGCTGTACAACTCTTGGTCCCTTTATGCCGCTGTATACCAATTTCTTT 660
Db 757 TGGGGCCCAAGCTGTACAACTCTTGGTCCCTTTATGCCGCTGTATACCAATTTCTTT 816
QY 661 TGTCTTTGGGTATACATTAA 681
Db 817 TGTCTTTGGGTATACATTAA 837

RESULT 3
US-10-453-792-286
; Sequence 286, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-Apr-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SAOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 286:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 286:
US-10-453-792-286
Query Match 97.9%; Score 666.6; DB 13; Length 3215;
Best Local Similarity 98.7%; Pred. No. 3.4e-207;
Matches 672; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ATGAGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTGCTGTGTACAGGGGGGTTTTC 60
Db 157 ATGAGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTGCTGTGTACAGGGGGGTTTTC 216
QY 61 TTGTTGACAAAATTCCTCAATACCCGACAGTCTAGACTCGTGTGGACTTCTCTCAAT 120
Db 217 TTGTTGACAAAATTCCTCAATACCCGACAGTCTAGACTCGTGTGGACTTCTCTCAAT 276
QY 121 TTCTAGGGGAAACACCGGTGTGCTTGGCCAAAATTCGAGATCCCAAAATTCAGATCAC 180
Db 277 TTCTAGGGGAAACACCGGTGTGCTTGGCCAAAATTCGAGATCCCAAAATTCAGATCAC 336
QY 181 TCACCAACCTGTTGCTCCTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 337 TCACCAACCTGTTGCTCCTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 396
QY 241 ATCATCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 397 ATCATCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 456
QY 301 CAAGGTATGTTGCCGTTTGTCTTAATTCAGGATCAACAAACAGACACCGGACCA 360
Db 457 CAAGGTATGTTGCCGTTTGTCTTAATTCAGGATCAACAAACAGACACCGGACCA 516
QY 361 TGCAAAACCTGCACAACTCCTGCTCAAGGACCTCTATGTTTCCCTCATGTTGCTGTACA 420
Db 517 TGCAAAACCTGCACAACTCCTGCTCAAGGACCTCTATGTTTCCCTCATGTTGCTGTACA 576
QY 421 AAACCTAGGACAGAACTGCACCTGTATTCCCATCCCATCATCTGGGCTTTTCGCAAAA 480
Db 577 AAACCTATGGATGGAACCTGCACCTGTATTCCCATCCCATCATCTGGGCTTTTCGCAAAA 636
QY 481 TACCTATGGAGTGGGCTTCAGTCCGTTTCTCTTGGCTCAGTCTTACTAGTGCCATTGTT 540
Db 637 TACCTATGGAGTGGGCTTCAGTCCGTTTCTCTTGGCTCAGTCTTACTAGTGCCATTGTT 696
QY 541 CAGTGTTCGTAGGCTTTCCCTCCACTGTCTGGCTTTTCAGTTATATGATGATGATGATGAT 600
Db 697 CAGTGTTCGTAGGCTTTCCCTCCACTGTCTGGCTTTTCAGTTATATGATGATGATGATGAT 756
QY 601 TGGGGCCCAAGCTGTACAACTCTGAGTCCCTTTATGCCGCTGTATACCAATTTCTTT 660
Db 757 TGGGGCCCAAGCTGTACAACTCTGAGTCCCTTTATGCCGCTGTATACCAATTTCTTT 816
QY 661 TGTCTTTGGGTATACATTAA 681
Db 817 TGTCTTTGGGTATACATTAA 837

RESULT 4
US-10-453-792-284
; Sequence 284, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON

STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 283:
SEQUENCE CHARACTERISTICS:
LENGTH: 3221 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 283:
US-10-453-792-283

Query Match 97.4%; Score 663.4; DB 13; Length 3215;
Best Local Similarity 98.4%; Pred. No. 3.8e-206;
Matches 670; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGAGAACATCGCATCAGGACTCTAGGACCCCTGCTGTGTACAGCGGGGTTTTC 60
DB 157 ATGAGAACATCGCATCAGGACTCTAGGACCCCTGCTGTGTACAGCGGGGTTTTC 216
QY 61 TTGTTGACAAATCTTCACAAATACCCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
DB 217 TCGTTGACAAATCTTCACAAATCTAGACTCGTGGTGGACTTCTCTCAAT 276
QY 121 TTCTTAGGGGAAACACCCGCTGCTCTGGCCAAATTCGAGTCCCAATATCCAGTCAAC 180
DB 277 TTCTTAGGGGAAACACCCGCTGCTCTGGCCAAATTCGAGTCCCAATATCCAGTCAAC 336
QY 181 TCACCAACCTGTTGCTCTCAATTTGCTGTTATCGCTGATGCTGCGGGGTTTTC 240
DB 337 TCACCAACCTGTTGCTCTCAATTTGCTGTTATCGCTGATGCTGCGGGGTTTTC 396
QY 241 ATCATCTCTCTGATCTCTGCTGCTATGCTCATCTCTTGTGTTGTTCTTCTGACTAT 300
DB 397 ATCATCTCTCTGATCTCTGCTGCTATGCTCATCTCTTGTGTTGTTCTTCTGACTAT 456
QY 301 CAAGGTATGTTGCCGTTGCTCTCAATTTGCTGATCAACAAACAGACCGGACCA 360
DB 457 CAAGGTATGTTGCCGTTGCTCTCAATTTGCTGATCAACAAACAGACCGGACCA 516
QY 361 TGCARAACTGCAACCTGCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 420
DB 517 TGCARAACTGCAACCTGCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 576
QY 421 AAACCTACGGACGAGAACTGCACCTGTATTTCCCATCCCATCATCTTTGGGCTTTGCAAAA 480
DB 577 AAACCTACGGACGAGAACTGCACCTGTATTTCCCATCCCATCATCTTTGGGCTTTGCAAAA 636

QY 481 TACCTATGGGAGTGGGCTCAGTCCGTTTCTTTGGCTCAGTTTACCTAGTGCCATTTGTT 540
DB 637 TACCTATGGGAGTGGGCTCAGTCCGTTTCTTTGGCTCAGTTTACCTAGTGCCATTTGTT 696
QY 541 CAGTGGTTCGTAGGCTTCCGCCACATCTGCTGGCTTTTCTAGTTATATGATGATGCTGTT 600
DB 697 CAGTGGTTCGTAGGCTTCCGCCACATCTGCTGGCTTTTCTAGTTATATGATGATGCTGTT 756
QY 601 TGGGGGCCAAGTCTGTACACATCTTGGTCCCTTTATGCGCTGTTTACCAATTTCTTT 660
DB 757 TGGGGGCCAAGTCTGTACACATCTTGGTCCCTTTATGCGCTGTTTACCAATTTCTTT 816
QY 661 TGTCTTTGGGTATACATTTAA 681
DB 817 TGTCTTTGGGTATACATTTAA 837

RESULT 5
US-10-453-792-283
; Sequence 283, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 283:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3221 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 284:
US-10-453-792-284

```

RESULT 6
US-10-365-620-33
; Sequence 33, Application US/10365620
; Publication NO. US20040001853A1
; GENERAL INFORMATION:
; APPLICANT: George, Rajan
; APPLICANT: Tyrell, Lorne
; APPLICANT: No US20040001853A1aim, Antoine
; TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response
; FILE REFERENCE: 656.0016
; CURRENT APPLICATION NUMBER: US/10/365,620
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US60/423,578
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: 60/390,564
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 33
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Hepatitis B virus
US-10-365-620-33

```

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RESULT 7
US-10-365-620-28
; Sequence 28, Application US/10365620
; Publication No. US20040001853A1
; GENERAL INFORMATION:
; APPLICANT: George, Rajan
; APPLICANT: Tyrrell, Lorne
; APPLICANT: NO. US20040001853Aljaim, Antoine
; TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response
; FILE REFERENCES: 656.0016
; CURRENT APPLICATION NUMBER: US/10/365,620
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US60/423,578
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: 60/390,564
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28

```

LENGTH: 2037
; TYPE: DNA
; ORGANISM: Hepatitis B virus
US-10-365-620-28

Query Match 92.9%; Score 632.6; DB 16; Length 2037;
Best Local Similarity 95.7%; Pred. No. 3.8e-196;
Matches 650; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 1 ATGAGAACATCGCATCAGGACTCTAGGACCCCTGCTGTTTACAGGCGGGTTTTTC 60
DB 607 ATGAGAACATCATCAGGATTCCTAGGACCCCTGCTGTTTACAGGCGGGTTTTTC 666
QY 61 TTGTTGACAAATTCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
DB 667 TTGTTGACAAATTCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 726
QY 121 TTCTAGGGGGAACACCCGCTGCTTGGCCAAATTCGCGAGTCCCAATCTCCAGTCAAC 180
DB 727 TTCTAGGGGGAACACCCGCTGCTTGGCCAAATTCGCGAGTCCCAATCTCCAGTCAAC 786
QY 181 TCACCAACCTCTGCTGCTCAATTTGCTGGTATCGCTGGATGCTGCGGCGTTTTT 240
DB 787 TCACCAACCTCTGCTGCTCAATTTGCTGGTATCGCTGGATGCTGCGGCGTTTTT 846
QY 241 ATCATCTCTCTGCTGCTCAATTTGCTGGTATCGCTGGATGCTGCGGCGTTTTT 300
DB 847 ATCATCTCTCTGCTGCTCAATTTGCTGGTATCGCTGGATGCTGCGGCGTTTTT 906
QY 301 CAAGGTATGTTGCCCGTTTGTCTCTAAATTCAGGATCAACCAACAGTACGGGACCA 360
DB 907 CAAGGTATGTTGCCCGTTTGTCTCTAAATTCAGGATCAACCAACAGTACGGGACCA 966
QY 361 TGCARAACTGCAACTCTGCTCAAGGAACTCTATGTTCCCTCATCTTGGGCTTTCGCAAAA 420
DB 967 TGCARAACTGCAACTCTGCTCAAGGAACTCTATGTTCCCTCATCTTGGGCTTTCGCAAAA 1026
QY 421 AAACCTACGACAGAACTGCACCTGTATTCATCCCATCATCTTGGGCTTTCGCAAAA 480
DB 1027 AAACCTACGACAGAACTGCACCTGTATTCATCCCATCATCTTGGGCTTTCGCAAAA 1086
QY 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTTGGCTCAGTCTTACTAGTGCATTTGTT 540
DB 1087 TACCTATGGAGTGGGCTCAGTCCGTTTCTTGGCTCAGTCTTACTAGTGCATTTGTT 1146
QY 541 CAGTGGTTCGTAGGGCTTTCCCGCTGCTGCTTTCAGTTATATGAGTATGATGTTT 600
DB 1147 CAGTGGTTCGTAGGGCTTTCCCGCTGCTGCTTTCAGTTATATGAGTATGATGTTT 1206
QY 601 TGGGGGCCAAGTCTGTACAGATCTGTAGTCCCTTTATGCGCTGTATACCAATTTCTTT 660
DB 1207 TGGGGGCCAAGTCTGTACAGATCTGTAGTCCCTTTATGCGCTGTATACCAATTTCTTT 1266
QY 661 TGTCTTTGGGTATACATTT 679
DB 1267 TGTCTTTGGGTATACATTT 1285

RESULT 8
US-10-365-620-31

; Sequence 31, Application US/10365620
; Publication No. US20040001853A1
; GENERAL INFORMATION:
; APPLICANT: George, Rajan
; APPLICANT: Tyrrell, Lorne
; APPLICANT: No. US20040001853A1, Antoine
; TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response
; FILE REFERENCE: 656 0016
; CURRENT APPLICATION NUMBER: US/10/365, 620
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US60/423, 578
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: 60/390, 564

; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 2037
; TYPE: DNA
; ORGANISM: Hepatitis B virus
US-10-365-620-31

Query Match 92.9%; Score 632.6; DB 16; Length 2037;
Best Local Similarity 95.7%; Pred. No. 3.8e-196;
Matches 650; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 1 ATGAGAACATCGCATCAGGACTCTAGGACCCCTGCTGTTTACAGGCGGGTTTTTC 60
DB 607 ATGAGAACATCATCAGGATTCCTAGGACCCCTGCTGTTTACAGGCGGGTTTTTC 666
QY 61 TTGTTGACAAATTCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
DB 667 TTGTTGACAAATTCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 726
QY 121 TTCTAGGGGGAACACCCGCTGCTTGGCCAAATTCGCGAGTCCCAATCTCCAGTCAAC 180
DB 727 TTCTAGGGGGAACACCCGCTGCTTGGCCAAATTCGCGAGTCCCAATCTCCAGTCAAC 786
QY 181 TCACCAACCTCTGCTGCTCAATTTGCTGGTATCGCTGGATGCTGCGGCGTTTTT 240
DB 787 TCACCAACCTCTGCTGCTCAATTTGCTGGTATCGCTGGATGCTGCGGCGTTTTT 846
QY 241 ATCATCTCTCTGCTGCTCAATTTGCTGGTATCGCTGGATGCTGCGGCGTTTTT 300
DB 847 ATCATCTCTCTGCTGCTCAATTTGCTGGTATCGCTGGATGCTGCGGCGTTTTT 906
QY 301 CAAGGTATGTTGCCCGTTTGTCTCTAAATTCAGGATCAACCAACAGTACGGGACCA 360
DB 907 CAAGGTATGTTGCCCGTTTGTCTCTAAATTCAGGATCAACCAACAGTACGGGACCA 966
QY 361 TGCARAACTGCAACTCTGCTCAAGGAACTCTATGTTCCCTCATCTTGGGCTTTCGCAAAA 420
DB 967 TGCARAACTGCAACTCTGCTCAAGGAACTCTATGTTCCCTCATCTTGGGCTTTCGCAAAA 1026
QY 421 AAACCTACGACAGAACTGCACCTGTATTCATCCCATCATCTTGGGCTTTCGCAAAA 480
DB 1027 AAACCTACGACAGAACTGCACCTGTATTCATCCCATCATCTTGGGCTTTCGCAAAA 1086
QY 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTTGGCTCAGTCTTACTAGTGCATTTGTT 540
DB 1087 TACCTATGGAGTGGGCTCAGTCCGTTTCTTGGCTCAGTCTTACTAGTGCATTTGTT 1146
QY 541 CAGTGGTTCGTAGGGCTTTCCCGCTGCTGCTTTCAGTTATATGAGTATGATGTTT 600
DB 1147 CAGTGGTTCGTAGGGCTTTCCCGCTGCTGCTTTCAGTTATATGAGTATGATGTTT 1206
QY 601 TGGGGGCCAAGTCTGTACAGATCTGTAGTCCCTTTATGCGCTGTATACCAATTTCTTT 660
DB 1207 TGGGGGCCAAGTCTGTACAGATCTGTAGTCCCTTTATGCGCTGTATACCAATTTCTTT 1266
QY 661 TGTCTTTGGGTATACATTT 679
DB 1267 TGTCTTTGGGTATACATTT 1285

RESULT 9

US-10-267-922-15
; Sequence 15, Application US/10267922
; Publication No. US20030143527A1
; GENERAL INFORMATION:
; APPLICANT: SHYAMALA, Venkatakrishna
; TITLE OF INVENTION: IDENTIFICATION OF OLIGONUCLEOTIDES FOR THE CAPTURE,
; TITLE OF INVENTION: DETECTION AND QUANTIFICATION OF HEPATITIS B VIRAL DNA
; FILE REFERENCE: 2301-18346 / PPI8346.004
; CURRENT APPLICATION NUMBER: US/10/267,922
; CURRENT FILING DATE: 2002-10-09

NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
COMPUTER READABLE FORM:
FILING DATE: 04-Jun-2003
APPLICATION NUMBER: US/10/453,792
CLASSIFICATION: <Unknown>
PRIORITY INFORMATION:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-Apr-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 280:
SEQUENCE CHARACTERISTICS:
LENGTH: 3200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 280:
US-10-453-792-280

Query Match 92.7%; Score 631.4; DB 13; Length 3200;
Best Local Similarity 95.4%; Pred. No. 1.2e-195;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 ATGGAGAACATCGCATCAGAGCTCCCTAGGACCCCTGCTGCTGTTACAGCGGGGTTTTTC 60
DB 157 ATGGAGAACATCAGATCAGAGATTCCTAGGACCCCTGCTGCTGTTACAGCGGGGTTTTTC 216
QY 61 TTGTTGACAAATACTCTCACAATACCGCAGAGTCTAGACTCGTGGTGACTTCTCTCAAT 120
DB 217 TTGTTGACAAAGATCTCTCACAATACCGCAGAGTCTAGACTCGTGGTGACTTCTCTCAAT 276
QY 121 TTCTAGGGGGAACACCCGTGTGTTGGCAAAATTCGAGTCCGAGTCCCAATCTCCAGTCAC 180
DB 277 TTCTAGGGGGAATCACCCTGTGTCTTGGCAAAATTCGAGTCCGAGTCCCAATCTCCAGTCAC 336
QY 181 TCACCAACCTGTGTGCTCCCAATTTGCTGCTGTTATCGTGGTGACTGCTGCGGGGTTTTT 240
DB 337 TCACCAACCTGTGTGCTCCCAATTTGCTGCTGTTATCGTGGTGACTGCTGCGGGGTTTTT 396
QY 241 ATCATCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 397 ATCATATCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 456
QY 301 CAAGGTATGTTCCCGGTTTGCTCTTAATTCAGATCAACAACACGACCGGACCA 360
DB 457 CAAGGTATGTTCCCGGTTTGCTCTTAATTCAGATCAACAACACGACCGGACCA 516
QY 361 TCACCAACCTGTGACAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 420

NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 1696
TYPE: DNA
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: exemplary
OTHER INFORMATION: Internal control sequence
US-10-267-922-15

Query Match 92.7%; Score 631.4; DB 15; Length 1696;
Best Local Similarity 95.4%; Pred. No. 8.5e-196;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 ATGGAGAACATCGCATCAGAGCTCCCTAGGACCCCTGCTGCTGTTACAGCGGGGTTTTTC 60
DB 7 ATGGAGAACATCAGATCAGAGATTCCTAGGACCCCTGCTGCTGTTACAGCGGGGTTTTTC 66
QY 61 TTGTTGACAAATACTCTCACAATACCGCAGAGTCTAGACTCGTGGTGACTTCTCTCAAT 120
DB 67 TTGTTGACAAAGATCTCTCACAATACCGCAGAGTCTAGACTCGTGGTGACTTCTCTCAAT 126
QY 121 TTCTAGGGGGAACACCCGTGTGTTGGCAAAATTCGAGTCCGAGTCCCAATCTCCAGTCAC 180
DB 127 TTCTAGGGGGAATCACCCTGTGTCTTGGCAAAATTCGAGTCCGAGTCCCAATCTCCAGTCAC 186
QY 181 TCACCAACCTGTGTGCTCCCAATTTGCTGCTGTTATCGTGGTGACTGCTGCGGGGTTTTT 240
DB 187 TCACCAACCTGTGTGCTCCCAATTTGCTGCTGTTATCGTGGTGACTGCTGCGGGGTTTTT 246
QY 241 ATCATCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 247 ATCATATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 306
QY 301 CAAGGTATGTTCCCGGTTTGCTCTTAATTCAGGATCAACAACACGACCGGACCA 360
DB 307 CAAGGTATGTTCCCGGTTTGCTCTTAATTCAGGATCAACAACACGAGTACGGGACCA 366
QY 361 TGCAAAACCTGTGCAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 420
DB 367 TGCAAAACCTGTGCAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 426
QY 421 AAACCTAGGACAGAACTGCACTGTAATTCCTATCCCATCCCATCTTGGGCTTTCGCAAA 480
DB 427 AAACCTAGGACAGAACTGCACTGTAATTCCTATCCCATCCCATCTTGGGCTTTCGCAAA 486
QY 481 TACTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 540
DB 487 TACTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 546
QY 541 CAGTGGTTCGTAGGGCTTTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 547 CAGTGGTTCGTAGGGCTTTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
QY 601 TGGGGGCAAGTCTGTACAACTCTTGGAGTCCCTTTATGCGGCTGTTTACCAATTTTCTTT 660
DB 607 TGGGGGCAAGTCTGTACAACTCTTGGAGTCCCTTTATGCGGCTGTTTACCAATTTTCTTT 666
QY 661 TGCTTTGGGTATACATTTAA 681
DB 667 TGCTTTGGGTATACATTTAA 687

RESULT 10
US-10-453-792-280
Sequence 280, Application US/10453/92
Publication No. US20040029110A1
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV

Db	517	TGCAAAACCTGCACAGCTCTCTGCTCAAGGCAACTCTAAGTTTCCCTCATGTCTGCTGTACA	576
Qy	421	AAACCTACGGACAGAAATGCACTGTATATCCCATCCCATCACTCTGGGCTTTGCAAAA	480
Db	577	AAACCTACGGATCGAAATGCACTGTATATCCCATCCCATCGCTCTGGGCTTTGCAAAA	636
Qy	481	TACCTATGGGAGTGGGCTCAGTCGGTTTCCTTGGCTCAGTTTACTATGTCGCATTGTT	540
Db	637	TACCTATGGGAGTGGGCTCAGTCGGTTTCCTTGGCTCAGTTTACTATGTCGCATTGTT	696
Qy	541	CAGTGTTCGTAGGCTTTCCCCCACTGTCTGGCTTTTCAGTTATATGGATGATGTGTTT	600
Db	697	CAGTGTTCGTAGGCTTTCCCCCACTGTTCAGTTATATGGATGATGTGTTT	756
Qy	601	TGGGGGCCAAGTCTGTACAAATCTTGAGTCCCTTTATGCCGCTGTATACCAATTTCTTT	660
Db	757	TGGGGGCCAAGTCTGTACAGCATGTGAGTCCCTTTATACCGCTGTTACCAATTTCTTT	816
Qy	661	TGCTTTTGGGTATACATTTAA	681
Db	817	TGCTCTCGGTATACATTTAA	837

RESULT 11

US-10-453-792-279
Sequence 279, Application US/10453792
Publication No. US20040029110A1
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSER: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD

Query Match	92.7%;	Score 631.4;	DB 13;	Length 3221;
Best Local Similarity	95.4%;	Pred. No. 1.2e-195;		
Matches 650;	Conservative 0;	Mismatches 31;	Indels 0;	Gaps 0;
Qy	1	ATGGAGAACATCGAATCAGAGACTCTTAGGACCCCTGCTGCTGTATCAGGCGGGGTTTTC	60	
Db	157	ATGGAGAACATCACATCAGGATTCCTTAGGACCCCTGCTGCTGTATCAGGCGGGGTTTTC	216	
Qy	61	TTGTTTGACAAAAATCCTCACAAATACCCGACAGAGCTAGACGCTGCTGGTGGAGCTTCTCTCAAT	120	
Db	217	TTGTTTGACAGAAATCCTCACAAATACCGACAGAGCTAGACGCTGCTGGTGGAGCTTCTCTCAAT	276	
Qy	121	TTTCTAGGGGGAACACCCGCTGTCTTTGGCCAAAATTCGCAGTCCCAAATCTCCAGTCAAC	180	
Db	277	TTTCTAGGGGGTACACCGCTGTCTTTGGCCAAAATTCGCAGTCCCAAATCTCCAGTCAAC	336	
Qy	181	TCACCAACCTGTTGTCTCTCCTCAATTTGTCTTGGTTATCGCTGGAGTGTCTGGCGGGTTTT	240	
Db	337	TCACCAACCTCTCTCTCTCCTCAATTTGTCTTGGTTATCGCTGGAGTGTCTGGCGGGTTTT	396	
Qy	241	ATCATCTTCTCTCTGCATCCTGCTCTATGCTCATCTTCTTGTGGTCTTCTCTGGACTAT	300	
Db	397	ATCATATTCTCTCTCACTGCTGCTATGCTCATCTTCTTGTGGTCTTCTCTGGACTAT	456	
Qy	301	CAAGGTATGTTGCCCGTTTGTCTCTAATTCAGGATCAACAAACACGACCCGGAACA	360	
Db	457	CAAGGTATGTTGCCCGTTTGTCTCTAATTCAGGATCAACAAACACGAGTACGGGAACA	516	
Qy	361	TGCAAAACCTGCAACAATCCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA	420	
Db	517	TGCAAAACCTGCAACAATCCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA	576	
Qy	421	AAACCTACGGGACGAAACATGCACTGTATTCCCATCCCATCATCTTGGGCTTCGCAAAA	480	
Db	577	AAACCTACGGGATGGAATTCGACCTGTATTCATCCCATCGTCTGGGCTTCGCAAAA	636	
Qy	481	TACCTATCGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTT	540	
Db	637	TACCTATCGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTT	696	
Qy	541	CAGTGGTTCTGTAGGGCTTTCCCCCACTGCTCGCTTTCAGTTATATGGAATGATGTGGTT	600	
Db	697	CAGTGGTTCTGTAGGGCTTTCCCCCACTGTTTGGCTTCAGCTATATGGAATGATGTGGTT	756	
Qy	601	TGGGGGCCAAGCTGTGTACAAACATCTTGAGTCCCTTTATGCGCTGTATACCAATTTCTTT	660	
Db	757	TGGGGGCCAAGCTGTGTACAGATCGTGAGTCCCTTTATACCGCTGTATACCAATTTCTTT	816	
Qy	661	TGCTTTTGGGTATACATTTAA	681	
Db	817	TGCTCTCGGTATACATTTAA	837	

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RESULT 12
US-09-781-891D-21
/ Sequence 21, Application US/09781891D
/ Publication No. US2003009622A1
/ GENERAL INFORMATION:
/ APPLICANT: Delaney, William IV
/ APPLICANT: Loccarnini, Stephen Alister
/ APPLICANT: Chen, Robert Yung Ming
/ APPLICANT: Bartholomewsz, Angeline
/ APPLICANT: Isom, Harriet
/ TITLE OF INVENTION: An assay
/ FILE REFERENCE: 2376750/EJH
/ CURRENT APPLICATION NUMBER: US/09/781,891D
/ CURRENT FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/179, 948
/ PRIOR FILING DATE: 2000-02-03
/ NUMBER OF SEQ IDS NOS: 22

```


CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/453,792
 FILING DATE: 04-Jun-2003
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/155,885A
 FILING DATE: 08-Oct-1998
 APPLICATION NUMBER: PCT/EP97/02002
 FILING DATE: 21-APR-1997
 APPLICATION NUMBER: EP 96870053.4
 FILING DATE: 19-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: SADOFF, B.J.
 REGISTRATION NUMBER: 36,663
 REFERENCE/DOCKET NUMBER: 2551-5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 304:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3182 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 SEQUENCE DESCRIPTION: SEQ ID NO: 304:
 US-10-453-792-304

Query Match 92.5%; Score 629.8; DB 13; Length 3182;
 Best Local Similarity 95.3%; Pred. No. 3.9e-195;
 Matches 649; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
 QY 1 ATGGAGAACATCGCATCAGGACTCTTAGGACCCCTGCTGTTACAGCGGGGTTTTC 60
 DB 157 ATGGAGAACATCATCAGGATTCCTAGGACCCCTGCTGTTACAGCGGGGTTTTC 216
 QY 61 TTGTTGACAAAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
 DB 217 TTGTTGACAGAAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 276
 QY 121 TTCTTAGGGGAAACACCGGTGTCTTGGCCAAAATTCGACGTCCCAATCTCCAGTCA 180
 DB 277 TTCTTAGGGGAACTACCGGTGTCTTGGCCAAAATTCGACGTCCCAATCTCCAGTCA 336
 QY 181 TCACCAACCTGTGTCCTCAATTTGCTGCTGTTATCGCTGGATGTCTGCGGGGTTTTC 240
 DB 337 TCACCAACCTGTGTCCTCAATTTGCTGCTGTTATCGCTGGATGTCTGCGGGGTTTTC 396
 QY 241 ATCATCTTCTCTGCAATCTGCTGATGCTCATCTTCTGTTGTTCTTCTGACTAT 300
 DB 397 ATCATCTTCTCTGCAATCTGCTGATGCTCATCTTCTGTTGTTCTTCTGACTAT 456
 QY 301 CAAGGTATGTGCGCGTTGTCCTCAATTTGCTGCTGTTATCGCTGGATGTCTGCGGGGTTTTC 360
 DB 457 CAAGGTATGTGCGCGTTGTCCTCAATTTGCTGCTGTTATCGCTGGATGTCTGCGGGGTTTTC 516
 QY 361 TGCAAAACCTGCAACTCTGCTCAAGGAACTCTATGTTTCCCTCATGTTGCTGTACA 420
 DB 517 TGCAGAACCTGCAAGACTCTGCTCAAGGAACTCTATGTTTCCCTCATGTTGCTGTACC 576

QY 421 AAACCTACGGACAGAAACTGCACCTGTATTCCCATCCATCATCTTGGGCTTTTCGAAAA 480
 DB 577 AAACCTTCGGACGGGAATTCACCTGTATTCCCATCCATCATCTTGGGCTTTTCGAAAA 636
 QY 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTACTAGTGCATTTGTT 540
 DB 637 TTCCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTACTAGTGCATTTGTT 696
 QY 541 CAGTGGTTCTGATGGGCTTTTCCCCACACTGTCTGGCTTTTTCAGTTATATGATGATGTTGTT 600
 DB 697 CAGTGGTTCTGATGGGCTTTTCCCCACACTGTCTGGCTTTTTCAGTTATATGATGATGTTGTT 756
 QY 601 TGGGGGCCAAGTCTGTACAACTTTGAGTCCCTTTTATGGCGTGTACCAATTTTCTTT 660
 DB 757 TGGGGGCCAAGTCTGTACAACTTTGAGTCCCTTTTATGGCGTGTACCAATTTTCTTT 816
 QY 661 TGTCTTTGGGTATACATTTAA 681
 DB 817 TGTCTCTGGGTATACATTTAA 837
 RESULT 15
 US-09-821-877-3
 ; Sequence 3, Application US/09821877
 ; Patent No. US2002017124A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Coleman, Paul F.
 ; APPLICANT: Mushalwar, Isa K.
 ; TITLE OF INVENTION: Hepatitis B Virus Surface Antigen Mutant
 ; TITLE OF INVENTION: And Methods Of Detection Thereof
 ; FILE REFERENCE: 6794.US.O1
 ; CURRENT APPLICATION NUMBER: US/09/821,877
 ; CURRENT FILING DATE: 2000-03-03
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 681
 ; TYPE: DNA
 ; ORGANISM: Hepatitis B Virus
 ; US-09-821-877-3

Query Match 92.2%; Score 628.2; DB 9; Length 681;
 Best Local Similarity 95.2%; Pred. No. 5.9e-195;
 Matches 648; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 QY 1 ATGGAGAACATCGCATCAGGACTCTTAGGACCCCTGCTGTTACAGCGGGGTTTTC 60
 DB 1 ATGGAGAACATCATCAGGATTCCTAGGACCCCTGCTGTTACAGCGGGGTTTTC 60
 QY 61 TTGTTGACAAAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
 DB 61 TTGTTGACAGAAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
 QY 121 TTCTTAGGGGAAACACCGGTGTCTTGGCCAAAATTCGACGTCCCAATCTCCAGTCA 180
 DB 121 TTCTTAGGGGAACTACCGGTGTCTTGGCCAAAATTCGACGTCCCAATCTCCAGTCA 180
 QY 181 TCACCAACCTGTGTCCTCAATTTGCTGCTGTTATCGCTGGATGTCTGCGGGGTTTTC 240
 DB 181 TCACCAACCTGTGTCCTCAATTTGCTGCTGTTATCGCTGGATGTCTGCGGGGTTTTC 240
 QY 241 ATCATCTTCTCTGCAATCTGCTGATGCTCATCTTCTGTTGTTCTTCTGACTAT 300
 DB 241 ATCATCTTCTCTGCAATCTGCTGATGCTCATCTTCTGTTGTTCTTCTGACTAT 300
 QY 301 CAAGGTATGTGCGCGTTGTCCTCAATTTGCTGCTGTTATCGCTGGATGTCTGCGGGGTTTTC 360
 DB 301 CAAGGTATGTGCGCGTTGTCCTCAATTTGCTGCTGTTATCGCTGGATGTCTGCGGGGTTTTC 360
 QY 361 TGCAAAACCTGCAACTCTGCTCAAGGAACTCTATGTTTCCCTCATGTTGCTGTACA 420

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Db      361  TGCAGAACCTGCACGACTCCTGCTCAAGGAACCTCTATGTATCCCTCCTGTTGCTGTACA 420
QY      421  AAACCTACGGACAGAAACTGCACCTGTATTCCTATCCCATCCCATCATCTTGGGCTTTCGCAAAA 480
Db      421  AAACCTTCGGATGGAAACTGCACCTGTATTCCTATCCCATCCCATCATCTTGGGCTTTCGCAAAA 480
QY      481  TACCTATGGGAGTGGGCTCAGTCCGCTTCTCTTGGCTCAGTTTACTAGTGCCATTGTT 540
Db      481  TTCTATGGGAGTGGGCTCAGCCGCTTCTCTTGGCTCAGTTTACTAGTGCCATTGTT 540
QY      541  CAGTGTTCGTAGGGCTTTCCTCCCACTGTCTGGCTTTCAGTTATATGGATGATGGTTT 600
Db      541  CAGTGTTCGTAGGGCTTTCCTCCCACTGTCTGGCTTTCAGTTATATGGATGATGGTTT 600
QY      601  TGGGGGCCAAGTCTGTACAACTCTTGGTCCCTTTATGCCGTGTACCAATTTTCCTT 660
Db      601  TGGGGGCCAAGTCTGTACAACTCTTGGTCCCTTTATGCCGTGTACCAATTTTCCTT 660
QY      661  TGTCTTTGGGTATACATTTAA 681
Db      661  TGTCTTTGGGTATACATTTAA 681
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Search completed: July 26, 2004, 16:40:02
Job time : 412 secs

OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 13:24:04 ; Search time 2410 Seconds
(without alignments)
8438.234 Million cell updates/sec

Title: US-09-719-533A-1_COPY_155_835
Perfect score: 681
Sequence: 1 ATGGAGACATCGCATCAGG.....GTCCTTGGGTATACATTAA 681

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfum:*
16: em_estom:*
17: em_ges_hum:*
18: em_ges_inv:*
19: em_ges_pln:*
20: em_ges_vrt:*
21: em_ges_fun:*
22: em_ges_mam:*
23: em_ges_mus:*
24: em_ges_pro:*
25: em_ges_rod:*
26: em_ges_phg:*
27: em_ges_vrl:*
28: gb_ges1:*
29: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	41.2	6.0	997	29	CNS005TE	AL060767 Drosophila
2	40.6	6.0	1201	13	BX376097	BX376097 BX376097
3	40.4	5.9	1201	13	BX460099	BX460099 BX460099
4	40	5.9	258	9	AV717959	AV717959 AV717959

C 5	40	5.9	258	9	AV717967	AV717967 AV717967
C 6	40	5.9	262	9	AV717947	AV717947 AV717947
C 7	40	5.9	264	9	AV717948	AV717948 AV717948
C 8	40	5.9	268	9	AV717975	AV717975 AV717975
C 9	40	5.9	269	9	AV717986	AV717986 AV717986
C 10	40	5.9	270	9	AV717995	AV717995 AV717995
C 11	40	5.9	270	9	AV718017	AV718017 AV718017
C 12	40	5.9	271	9	AV717964	AV717964 AV717964
C 13	40	5.9	300	9	AV717969	AV717969 AV717969
C 14	40	5.9	301	9	AV718014	AV718014 AV718014
C 15	40	5.9	301	9	AV718019	AV718019 AV718019
C 16	40	5.9	310	9	AV717951	AV717951 AV717951
C 17	40	5.9	314	9	AV718022	AV718022 AV718022
C 18	40	5.9	315	9	AV717996	AV717996 AV717996
C 19	40	5.9	334	9	AV718004	AV718004 AV718004
C 20	39.8	5.8	520	28	BZ128636	BZ128636 CH230-440
C 21	39.8	5.8	636	28	AZ038456	AZ038456 RPCI-23-2
C 22	39.6	5.8	1200	9	AL576292	AL576292 AL576292
C 23	39.6	5.8	1201	9	AL563860	AL563860 AL563860
C 24	39.2	5.8	802	12	EG921060	EG921060 602825311
C 25	39.2	5.8	922	13	BX332924	BX332924 BX332924
C 26	39	5.7	382	10	BE003197	BE003197 QV4-BN009
C 27	38.8	5.7	1167	29	CNS04X6K	AL311285 Tetradon
C 28	38.6	5.7	611	14	CB580512	CB580512 AMGNNUC:C
C 29	38.6	5.7	628	13	BX482821	BX482821 DKFZp686B
C 30	38.6	5.7	1155	10	BF570907	BF570907 602076093
C 31	38.4	5.6	239	10	BF778098	BF778098 NXSI 077
C 32	38.4	5.6	264	9	AV717955	AV717955 AV717955
C 33	38.4	5.6	409	9	AI113181	AI113181 UI-R-C2p-
C 34	38.4	5.6	621	12	BM492837	BM492837 NXRV 031
C 35	38.4	5.6	705	12	BM902701	BM902701 NXLV 057
C 36	38.2	5.6	214	9	AI053945	AI053945 qi71h02.x
C 37	38.2	5.6	528	10	BE978648	BE978648 bs81c02.y
C 38	38.2	5.6	598	29	CE376635	CE376635 tigr-gss-
C 39	38	5.6	312	9	AV718005	AV718005 AV718005
C 40	38	5.6	1159	13	BX394939	BX394939 BX394939
C 41	37.8	5.6	887	13	BU217345	BU217345 603754791
C 42	37.6	5.5	397	14	T89211	T89211 yel12b04.r1
C 43	37.6	5.5	918	13	BQ710077	BQ710077 AGENCOURT
C 44	37.6	5.5	1085	12	EG293693	EG293693 602390570
C 45	37.6	5.5	1101	29	CNS01844	AL108862 Drosophil

ALIGNMENTS

RESULT 1
CNS005TE
LOCUS
DEFINITION
CNS005TE 997 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR12K22 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL060767.1 GI:4943573
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 997)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of

Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : liangellifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS09F010DH050P1.

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Location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF010Y12"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

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[illegible]

AV717959 258 bp mRNA linear EST 21-OCT-2003
 AV717959 GK Homo sapiens CDNA clone F0KABB05 5', mRNA sequence.
 AV717959
 AV717959.2 GI:37805005
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 258)
 Wu,T., Qian,B., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z.,
 Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
 Zeng,L., Xu,S., Gu,W., Tia,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
 Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
 Homo sapiens cDNA GK clones
 Unpublished (2000)
 On Oct 16, 2000 this sequence version replaced gi:10815111.
 Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex.45)
 Fax: 86-21-50801922
 Email: hanzgc@hgc.sh.cn
 This clone is available at CHGC in Shanghai.

AV171959 GK Homo sapiens CDNA clone FGKAB95 5', mRNA sequence.
AV171959
AV171959.2 GI:37805005
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 258)
Wu, T., Qian, B., Huang, Q., Huang, C., Kang, B., Gao, X., Xu, Z.,
Xiao, H., Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z.,
Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M.,

Lu, G., Yang, Y., Gu, Y., Chen, Z. and Han, Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2003 this sequence version replaced gi:10815111.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.

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RESULT 6
AV717947/c
LOCUS             AV717947             262 bp      mRNA      linear      EST 21-OCT-2003
DEFINITION       AV717947 GK Homo sapiens cDNA clone FGKABAH01 5', mRNA sequence.
ACCESSION        AV717947
VERSION          AV717947.2   GI:37804993
KEYWORDS         EST.
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS          Wu,T., Qian,B., Huang,Q., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815099.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzgchgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source           Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FGKABAH01"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="GK"
/clone_lib="GK"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match      5.9%; Score 40; DB 9; Length 262;
Best Local Similarity 100.0%; Pred.No. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 496 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTCCCAT 535
Db 262 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTCCCAT 225

RESULT 7
AV717948/c
LOCUS             AV717948             264 bp      mRNA      linear      EST 21-OCT-2003
DEFINITION       AV717948 GK Homo sapiens cDNA clone FGKABAH03 5', mRNA sequence.
ACCESSION        AV717948
VERSION          AV717948.2   GI:37804994
KEYWORDS         EST.
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS          Wu,T., Qian,B., Huang,Q., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815100.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzgchgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source           Location/Qualifiers
1..264
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FGKABAH03"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="GK"
/clone_lib="GK"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match      5.9%; Score 40; DB 9; Length 264;
Best Local Similarity 100.0%; Pred.No. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 496 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTCCCAT 535
Db 262 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTCCCAT 223

RESULT 8
AV717975/c
LOCUS             AV717975             268 bp      mRNA      linear      EST 21-OCT-2003
DEFINITION       AV717975 GK Homo sapiens cDNA clone FGKABAH12 5', mRNA sequence.
ACCESSION        AV717975
VERSION          AV717975.2   GI:37805020
KEYWORDS         EST.
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS          Wu,T., Qian,B., Huang,Q., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815127.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzgchgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source           Location/Qualifiers
1..268
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FGKABAH12"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="GK"
/clone_lib="GK"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match      5.9%; Score 40; DB 9; Length 268;
Best Local Similarity 100.0%; Pred.No. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 496 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTCCCAT 535

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Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzgchgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1..264
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FGKABAH03"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="GK"
/clone_lib="GK"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match      5.9%; Score 40; DB 9; Length 264;
Best Local Similarity 100.0%; Pred.No. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 496 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTCCCAT 535
Db 264 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTCCCAT 225

RESULT 8
AV717975/c
LOCUS             AV717975             268 bp      mRNA      linear      EST 21-OCT-2003
DEFINITION       AV717975 GK Homo sapiens cDNA clone FGKABAH12 5', mRNA sequence.
ACCESSION        AV717975
VERSION          AV717975.2   GI:37805020
KEYWORDS         EST.
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS          Wu,T., Qian,B., Huang,Q., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815127.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzgchgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source           Location/Qualifiers
1..268
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FGKABAH12"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="GK"
/clone_lib="GK"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match      5.9%; Score 40; DB 9; Length 268;
Best Local Similarity 100.0%; Pred.No. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 496 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTCCCAT 535

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Db      268 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTGCCAT 229
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AV717986      269 bp      mRNA      linear      EST 21-OCT-2003
AV717986 GK Homo sapiens cDNA clone FGKABAF01 5', mRNA sequence.
AV717986
AV717986.2 GI:37805031
EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 269)
AUTHORS     Wu,T., Qian,B., Huang,Q., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
TITLE      Homo sapiens cDNA GK clones
JOURNAL     Unpublished (2000)
COMMENT     On Oct 16, 2000 this sequence version replaced gi:10815138.
Contact: Zeguaguan Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES             source
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                        /clone_lib="GK"
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                        XhoI"

ORIGIN
Query Match      5.9%; Score 40; DB 9; Length 269;
Best Local Similarity 100.0%; Pred. NO. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      496 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTGCCAT 535
|||||
DB      269 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTGCCAT 231
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RESULT 10
AV717995/c
LOCUS      AV717995 GK Homo sapiens cDNA clone FGKABAF08 5', mRNA sequence.
DEFINITION AV717995
ACCESSION  AV717995
VERSION    AV717995.2 GI:37805038
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 270)
AUTHORS     Wu,T., Qian,B., Huang,Q., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
TITLE      Homo sapiens cDNA GK clones
JOURNAL     Unpublished (2000)
COMMENT     On Oct 16, 2000 this sequence version replaced gi:10815147.
Contact: Zeguaguan Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES             source
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                        /organism="Homo sapiens"
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                        XhoI"

ORIGIN
Query Match      5.9%; Score 40; DB 9; Length 269;
Best Local Similarity 100.0%; Pred. NO. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      496 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTGCCAT 535
|||||
DB      269 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTGCCAT 230
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RESULT 10
AV717995/c
LOCUS      AV717995 GK Homo sapiens cDNA clone FGKABAF08 5', mRNA sequence.
DEFINITION AV717995
ACCESSION  AV717995
VERSION    AV717995.2 GI:37805038
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 270)
AUTHORS     Wu,T., Qian,B., Huang,Q., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
TITLE      Homo sapiens cDNA GK clones
JOURNAL     Unpublished (2000)
COMMENT     On Oct 16, 2000 this sequence version replaced gi:10815147.
Contact: Zeguaguan Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES             source
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                        /dev_stage="Adult"
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                        /clone_lib="GK"
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                        XhoI"

ORIGIN
Query Match      5.9%; Score 40; DB 9; Length 270;
Best Local Similarity 100.0%; Pred. NO. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      496 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTGCCAT 535
|||||
DB      270 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTGCCAT 231
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RESULT 11
AV718017/c
LOCUS      AV718017 GK Homo sapiens cDNA clone FGKABAE09 5', mRNA sequence.
DEFINITION AV718017
ACCESSION  AV718017
VERSION    AV718017.2 GI:37805058
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 270)
AUTHORS     Wu,T., Qian,B., Huang,Q., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
TITLE      Homo sapiens cDNA GK clones
JOURNAL     Unpublished (2000)
COMMENT     On Oct 16, 2000 this sequence version replaced gi:10815169.
Contact: Zeguaguan Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES             source
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                        /organism="Homo sapiens"
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                        /clone="FGKABAE09"
                        /tissue_type="hepatocellular carcinoma"
                        /dev_stage="Adult"
                        /lab_host="SOLR"
                        /clone_lib="GK"
                        /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                        XhoI"

ORIGIN
Query Match      5.9%; Score 40; DB 9; Length 270;
Best Local Similarity 100.0%; Pred. NO. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      496 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTGCCAT 535
|||||
DB      270 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTGCCAT 231
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```

```

Contact: Zeguaguan Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES             source
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                        /organism="Homo sapiens"
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                        /dev_stage="Adult"
                        /lab_host="SOLR"
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                        XhoI"

ORIGIN
Query Match      5.9%; Score 40; DB 9; Length 270;
Best Local Similarity 100.0%; Pred. NO. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      496 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTGCCAT 535
|||||
DB      270 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTGCCAT 231
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RESULT 11
AV718017/c
LOCUS      AV718017 GK Homo sapiens cDNA clone FGKABAE09 5', mRNA sequence.
DEFINITION AV718017
ACCESSION  AV718017
VERSION    AV718017.2 GI:37805058
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 270)
AUTHORS     Wu,T., Qian,B., Huang,Q., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
TITLE      Homo sapiens cDNA GK clones
JOURNAL     Unpublished (2000)
COMMENT     On Oct 16, 2000 this sequence version replaced gi:10815169.
Contact: Zeguaguan Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES             source
  source              1..270
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="FGKABAE09"
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                        /dev_stage="Adult"
                        /lab_host="SOLR"
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                        XhoI"

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Best Local Similarity 100.0%; Pred. NO. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      496 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTGCCAT 535
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DB      270 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTGCCAT 231
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Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 535
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Db 270 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 231
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RESULT 12
AV717964/c
LOCUS AV717964 GK Homo sapiens cDNA clone FKGAB08 5', mRNA linear EST 21-OCT-2003
DEFINITION AV717964 GK Homo sapiens cDNA clone FKGAB08 5', mRNA sequence.
ACCESSION AV717964
VERSION AV717964.2 GI:37805010
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 271)
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,F., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815116.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..271
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/db_xref="taxon:9606"
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/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GK"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

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Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 535
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Db 271 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 232
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RESULT 13
AV717969/c
LOCUS AV717969 GK Homo sapiens cDNA clone FKGAB04 5', mRNA linear EST 21-OCT-2003
DEFINITION AV717969 GK Homo sapiens cDNA clone FKGAB04 5', mRNA sequence.
ACCESSION AV717969
VERSION AV717969.2 GI:37805015
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 300)
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,F., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815116.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
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/clone="FGKAB04"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
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/clone_lib="GK"
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XhoI"

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RESULT 14
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LOCUS AV718014 GK Homo sapiens cDNA clone FKGABAF12 5', mRNA linear EST 21-OCT-2003
DEFINITION AV718014 GK Homo sapiens cDNA clone FKGABAF12 5', mRNA sequence.
ACCESSION AV718014
VERSION AV718014.2 GI:37805056
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 301)
Wu,T., Qian,B., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,F., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815166.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..301
/organism="Homo sapiens"
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/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GK"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 5.9%; Score 40; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 535
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Db 300 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 261
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RESULT 15
AV718014/c
LOCUS AV718014 GK Homo sapiens cDNA clone FKGABAF12 5', mRNA linear EST 21-OCT-2003
DEFINITION AV718014 GK Homo sapiens cDNA clone FKGABAF12 5', mRNA sequence.
ACCESSION AV718014
VERSION AV718014.2 GI:37805056
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 301)
Wu,T., Qian,B., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,F., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815166.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
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/lab_host="SOLR"
/clone_lib="GK"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 5.9%; Score 40; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 535
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Db 300 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 261
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Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815121.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
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XhoI"

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Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 535
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Db 300 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 261
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RESULT 14
AV718014/c
LOCUS AV718014 GK Homo sapiens cDNA clone FKGABAF12 5', mRNA linear EST 21-OCT-2003
DEFINITION AV718014 GK Homo sapiens cDNA clone FKGABAF12 5', mRNA sequence.
ACCESSION AV718014
VERSION AV718014.2 GI:37805056
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 301)
Wu,T., Qian,B., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,F., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815166.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..301
/organism="Homo sapiens"
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/dev_stage="Adult"
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/clone_lib="GK"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 535
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Db 300 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 261
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ORIGIN XhoI

Query Match 5.9%; Score 40; DB 9; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 GCCTCAGTCGGTTCTCTGGCTCAGTTTACTAGTGCCAT 535
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Db 301 GCCTCAGTCGGTTCTCTGGCTCAGTTTACTAGTGCCAT 262

RESULT 15

AV718019/c
LOCUS AV718019 GK Homo sapiens cDNA clone FGAABC02 5', mRNA linear EST 21-OCT-2003
DEFINITION AV718019
ACCESSION AV718019
VERSION AV718019.2 GI:37805060
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Wu, T., Qian, B., Huang, Q., Kang, B., Gao, X., Xu, Z.,
Xiao, H., Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z.,
Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M.,
Lu, G., Yang, Y., Gu, Y., Chen, Z. and Han, Z.

TITLE

Homo sapiens cDNA GK clones
JOURNAL Unpublished (2000)

COMMENT

On Oct 16, 2000 this sequence version replaced gi:10815171.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@hgsc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

Source
1..301
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FGAABC02"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GK"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

Query Match 5.9%; Score 40; DB 9; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 GCCTCAGTCGGTTCTCTGGCTCAGTTTACTAGTGCCAT 535
|||||
Db 301 GCCTCAGTCGGTTCTCTGGCTCAGTTTACTAGTGCCAT 262

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Job time : 2413 secs

